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SEARCH REQUEST FORM

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Scientific and Technical Information Center

Requester's Full Name: OT 161/2 Art Unit: 11.42 Phone Nu Mail Box and Bldg/Room Location:	, <i>LEO</i> Ember 30 <u>G 3 4 5 CM 9 A 11 3</u> Results	Examiner #: 72967 Date://29/02 Serial Number: 09/60366 Format Preferred (circle): PAPER DISK E-MAIL
Include the elected species or structures, key	arch topic, and describe as words, synonyms, acronyn at may have a special mean	**************************************
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Inventors (please provide full names):	-	
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Sequences AAW95463-471 represent LS170 polypeptide fragments which CC contain at least on epitope in their sequences. The present invention CC relates to detection of a target LS170 polypucleotide that comprises treating a test sample with at least one LS170-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAXO0801-09) CC which are fragments derived from various clones of LS170 gene. The LS170 nucleic acid fragments represent a set of contiguous, partially CC overlapping sequences transcribed from lung tissue. They are used for CC diagnosis, staging, monitoring, in vivo imaging, prevention and treatment CC in ung disease, specifically cancer, and to indicate predisposition to such disease, specifically cancer, and to indicate predisposition to Such disease. Particularly detection of LS170 polynucleotide, LS170 antigens, or anti-LS170 antibodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening, LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in
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                                                                       Sequences AAW95463-471 represent LS170 polypeptide fragments which contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polypucleotide that comprises treating a test sample with at least one LS170 specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LS170 gene. The LS170 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease, specifically cancer, and to indicate predisposition to such disease. Particularly detection of LS170 polypucleotide, LS170 antipens, or anti-LS170 antibodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid
          sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in assays; as targets for drug screening, and as components or targets for
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                                                                                                                                                                                                                                                                                                                                                                      New LS170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
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RESULT
AAW95471
                                                        Sequences AAW95463-471 represent LS170 polypeptide fragments which contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polypucleotide that comprises treating a test sample with at least one LS170-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LS170 gene. The LS170 culleic acid fragments represent a set of contiguous, partially converlapping sequences transcribed from lung tissue. They are used for coverlapping sequences transcribed from lung tissue. They are used for content of lung disease, specifically cancer, and to indicate predisposition to such disease. Particularly detection of LS170 polynucleotide, LS170 cantigens, or anti-LS170 antibodies is indicative of disease. Cells care used to expression system comprising the LS170 nucleic acid con be used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in the polypeptides. The polypeptides of the sequences are as anti-care of ring screening, and as components or targets for Ab an heavy sequences.
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                       used
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Gordon J, Granadosen,
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                     used to deliver therapeutic agents to LS170-expressing cells; directly
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therapeutic
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disease, particularly

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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-032366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          competitive binding drug screens, and to generate antibodies for use in rational drug design.
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                                                                                   The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived
                                                                                                                                                                                                         Penn
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                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder.
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                                               Sequence
                                                                                                                                      Claim
                                                                                                                                                                   Human
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                                                                                                                                      27;
                                                                                                                                                       genome-derived single exon nucleic acid probes useful zing gene expression in human placenta .
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                                                                            placenta. The probes are useful for
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red. No. 86;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                               AAM30376;
                                                                                                                     AAM30376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 22695; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer
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26-MAY-2000;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                               (first entry)
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2000US-0207456.
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                                                                                                                        Protein; 93
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                   .6e+02;
                                                                                                                                                                                                                                                                                                                                                                         Length 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             part of the printed directly from WIPO
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AAM05518
ID AAM0
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Best Local :
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                                     09-AUG-2001.
                                                         WO200157270-A2
                                                                                           Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
                                                                                                                            Peptide #4200
                                                                                                                                               09-OCT-2001
                                                                           Homo sapiens.
                                                                                                                                                                   AAM05518;
                                                                                                                                                                                    AAM05518 standard;
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn
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27-SEP-2000;
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03-AUG-2000;
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26 - MAY - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 30645; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
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nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                            93 AA;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                     Protein;
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Pred.
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                                                                                                                        for measuring breast gene expression.
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1.6e+02;
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                                                                                            non-carcinoma tumour.
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04-FEB-2000; 2000US-0180312 29-JAN-2001; 2001WO-US00661.

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RESULT
AAY06408
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Best Local S
Matches 6
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 14258; 322pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in a
                                                                                                                                                                                                    diagnosis
                                                                                                                                                                                                                                                                                                           AAY06408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel
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27-SEP-2000;
30-DEC-1998;
02-JAN-1998;
                                  31-DEC-1998;
                                                                                W09935252-A2
                                                                                                                  Protein
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                              Secreted protein; nh796_1; human; brain; thalamus; therapy;
                                                                                                                                                                                                                                     Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conserv
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                    protein nh796_1.
98US-0222653
98US-0070346
                                  98WO-US27903
                                                                                                     /note= "predicted leader/signal sequence" 20..256 /note= "mature protein"
                                                                                                                                         Location/Qualifiers 7..19
                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No. 1.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe used to measuring gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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1.6e+02;
hes 0;
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Best Local S
Matches 6
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N-PSDB; AAX59356.
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                                                                                          Gordon J, Granadosen, Hodgo
Roberts-rapp L, Russell JC,
                                                                                                                       Billing-medel PA, Gordon J, Granad
                                                                                                                                                                                                                                                                                                11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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                       N-PSDB; AAX00809
                                             WPI; 1999-060335/05
                                                                                                                                                                                              (ABBO ) ABBOTT
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                                                                                                                                                                                                 LAB.
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                                                                                                                       n M, Colpitts TL,
Hodges SC, Klass
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                                                                                               Stroupe SD;
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Pred. No.
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                                                                                                                         MR,
                                                                                                                                               Friedman PN;
                                                                                                                         Kratochvil JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAW95463-471 represent LS170 polypeptide fragments which CC contain at least on epitope in their sequences. The present invention CC relates to detection of a target LS170 polynucleotide that comprises CC treating a test sample with at least one LS170-specific nucleic acid that CC which are fragments derived from various clones of LS170 gene. The LS170 coverlaping sequences transcribed from lung tissue. They are used for CC diagnosis, staging, monitoring, in vivo imaging, prevention and treatment CC of lung disease, specifically cancer, and to indicate predisposition to coverlapens, or anti-LS170 antibodies is indicative of disease. Cells CC transformed with an expression system comprising the LS170 nucleic acid cequences are used to express recombinant polypeptides. The polypuctides are used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as stargets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can be competitive binding drug screens, and to generate anti-idiotypic competitive binding drug screens, and to generate anti-idiotypic competitive binding drug screens, and to generate anti-idiotypic competitive binding drug screens, and to generate anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
     Lung specific genes for developing products for diagnosing, monitoring, staging, prognosticating, imaging and treating lung cancer
                                                                                                                                                                          04-AUG-1998;
                                                                                                                                                                                                         19-JUL-1999;
                                                                                                                                                                                                                                        17-FEB-2000.
                                                                                                                                                                                                                                                                        WO200008206-A1
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                      Lung specific
                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69164 standard; Protein; 256
                                                                                                                                           (DIAD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 96-97; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New LS170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 gggtsg 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGTSG 6
                                                          2000-195589/17.
DB: AAZ61165.
                                                                                                                                         DIADEXUS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                         Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                         98US-0095233
                                                                                                                                                                                                       99WO-US16247
                                                                                                         Recipon
                                                                                                                                                                                                                                                                                                                                lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                         Macina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 20;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
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RESULT 11
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Best Local S
Matches
                                                                                                                                                                                                                                                21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                           Zhao
                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotkinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is encoded by a lung specific gene, designated Lng110, clone ID 135520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer, especially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for
                                                                                                                                    Tang
                                                                                                                                                                                              14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                        19-JUL-2000;
03-AUG-2000;
                                                                                                                                                           (HYSE-)
                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM39721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM39721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 35-36; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 gggtsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGTSG
                                                                                                          A, ra
                                                                      2001-442253/47.
DB; AAI58877.
                                                                                                         Liu C,
Wang Z,
Zhou P,
                                                                                                                                                           HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA;
                                                                                                                                                                                 2000US-0488725.

2000US-0552317.

2000US-05538042.

2000US-0623312.

2000US-062312.

2000US-0653450.

2000US-0662191.

2000US-0693036.

2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                      Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2866
                                                                                                           Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                         72
                                                                                                         Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 21;
Pred. No. 3.8e+02;
Mismatches 0;
                                                                                                                    Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                    Ren F,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                    ۲.
                                                                                                                                Wang D;
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Example 4;

SEQ ID

NO 2866; 10078pp; English

such as

Novel nucleic acids and

ucleic acids and polypeptides, useful central nervous system injuries -

for

treating disorders

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AAB97366
ID AABS
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                      gene
                                                                                                                                                                                                                   Polynucleotide encoding LUNX gene product useful for cancer especially micrometastatic cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001078772-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUNX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB97366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB97366 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                      sequence
                                                                                                                                         This invention relates
                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-2001
                                                         diagnosis of micrometastatic cancer and for the production of the
                                                                                                 polynucleotide,
                                                                                                                                                                                                                                                                                                                                           (SAKA ) OTSUKA
                                                                            that binds to LUNX. The gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .N.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to human nucleic acids (AAIS7798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||
| gggtsg 85
                                   product. The present
                                                                                                                                                                                                                                                                                                     2001-313367/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUNX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
6; Conserv
                                                                                                                                                                                                                                                                                AAH27756,
                                                                                               ention relates to the human LUNX protein and the polynucleotide encoding it. The invention includes a vector containing a LUNX eotide, a host cell transformed with the vector, and an antibody
                                                                                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 AA;
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                             PHARM
                                                                                                                                                                                                                                                                                                                                                                                   99JP-0253186
                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0253186
                                                                                                                                                                           30pp; Japanese
                                                                                                                                                                                                                                                                                AAH27757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                             CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          micrometastatic
                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256
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Pred. No. 3.8
0; Mismatches
                                                                            can be used for cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
                                      represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not form part
                                        human LUNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                            the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256;
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                                                                                                 antibody
                                                             LUNX
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Query Match Best Local Similarity

100 0.0%;

Score Pred.

No.

DB 22; 3.8e+02;

Length 256;

specification

.N.S

disorders. The sequence

data

for this

patent

did not

form

part of the printed

lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, heamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and

immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAN38642-AAM42213) with nootropic,

and

Sequence

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1507
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19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                    Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM41507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM41507 standard; Protein;
                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                   WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2001
                                                                                                                                                                                                                                                                                 21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                      26-DEC-2000;
                                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                           peripheral
                                                                                                                                                   Novel nucleic acids and such as central nervous
                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                               leukaemia.
                                                                                                                                     Example
                                                                                                                                                                                              Zhao
                                                                                                                                                                                                                         (HYSE-)
                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                      14-SEP-2000;
                                                                                                                                                                                                                                               19-0CT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                  nootropic;
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                                                                                                                                     2; SEQ ID
                                                                                                                                                                        AAI60663
                                                                                                                                                                                                                          HYSEQ
                                                                                                                                                                                                    Liu
Wang
                                                                                                                                                                                                                                                                                                                                                                                          nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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                                                                                                                                                                                                                                             2000US-0488725.
2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0623450.
2000US-0662191.
2000US-0693036.
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u P,
                                                                                                                                                                                                                                         2000US-0727344
                                                                                                                                                                                                                                                                                                      2000WO-US34263
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                                                                                                                                                                                             Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressant;
                                                                                                                                     NO 6438; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           system;
                                                                                                                                                   polypeptides, useful system injuries -
                                                                                                                                                                                                                                                                                                                                                                                          neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                 6438
                                                                                                                                                                                                                                                                                                                                                                                                                                                           264
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                                                                                                                                                                                                     Xu C,
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Ku C, Xue
Drmanac R
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                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; cancer;
property; central nervous system; CNS;
                                                                                                                                                                                            e AJ,
                                                                                                                                                                                                    Qian >
                                                                                                                                                            for
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                                                                                                                                                                                                                                                                                                                                                                                            nervous system;
                                                                                                                                                            treating disorders
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                                                                                                                                                                                                    Ren F,
Zhang
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Best Local S
Matches 6
  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, hemocractic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S
                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                   Tang
Wang
Zhao
                                                                                                                                                                                             Example 2;
                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - {\bf r}
                                                                                                                                                                                                                                                            N-PSDB; AAI60945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                    (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM41789 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGTSG
                                                                                                                                                                                                                                                                         2001-442253/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic;
                                                                                                                                                                                                                                                                                                                                                    HYSEQ INC
                                                                                                                                                                                                                                                                                                 Wang z
Zhou
                                                                                                                                                                                                                                                                                         Liu C, Ye, Ye
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6; Conser
                                                                                                                                                                                             SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                           2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0662191
2000US-0693036
2000US-0727344
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ilarity 100.0%;
Conservative (
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2000US-0552317.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressant;
                                                                                                                                                                                                                                                                                                Goodrich R,
                                                                                                                                                                                         6720; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO
                                                                                                                                                                                                                                                                                             Chen R, Ma Y,
, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6720.
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Pred. No. 3.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
.9e+02;
                                                                                                                                                                                                                                                                                                         Qian xB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 264;
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                                                                                                                                                                                                                                                                                                         Ren F, V
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                      Wang D;
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RESULT :
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     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                          WPI; 2001-442253/47.
N-PSDB; AAI60946.
                                                                                                                                Example
                                                                                                                                                     Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                              (HYSE-)
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||
||123 gggtsg
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                                                                                                                             2; SEQ ID NO 6721; 10078pp; English.
                                                                                                                                                                                                                            Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                              HYSEQ
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6; Conserv
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2000US-0552317
2000US-0598042
2000US-0620312
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0693036
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Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug screening; arthritis; inflammation,
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Pred. No. 4e+02;
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lu C, Xue
Drmanac R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                            e AJ,
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                treating disorders
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Zhang J;
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lateral sch utilisation

Immune system suppression,

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Best Local S
Matches 6
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Note: The sequence data for this patent did not form part of the printed apperification.
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
01-APR-1999;
01-APR-1999;
16-APR-1999;
17-APR-1999;
21-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
24-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG11577 standard; Protein; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG11577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein identification; signal transduction pathway; metabolic
hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
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Local Similarity 100.
hes 6; Conservative
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|123 gggtsg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      2000EP-0301439
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 99US-0125788.
99US-0126785.
99US-0127462.
99US-012834.
99US-012834.
99US-0130871.
99US-0130871.
99US-0130871.
99US-0130871.
99US-0130871.
99US-013248.
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Pred. No. 4e+02;
Mismatches 0;
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promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
       25-MAY 1999;
27-MAY 1999;
28-MAY 1999;
01-JUN 1999;
01-JUN 1999;
10-JUN 1999;
11-JUN 1999;
11-JU
       990S-0136021
990S-0136392
990S-0136782
990S-0137528
990S-0137502
990S-0137502
990S-0139502
990S-0139453
990S-0139453
990S-0139453
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990S-0139461
990S-0139462
990S-0139463
990S-0140853
990S-0140853
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990S-0144333
990S-0144332
990S-0144333
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PR
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Best Local S
Matches 6
  25-FEB-1999
05-MAR-1999
05-MAR-1999
05-MAR-1999
25-MAR-1999
25-MAR-1999
26-APR-1999
16-APR-1999
16-APR-1999
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21-APR-1999
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23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-MAY-1999
25-MAY-1999
30-APR-1999
30-APR-1999
11-MAY-1999
11-JUN-1999
01-JUN-1999
01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000;
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29-OCT-1999;
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|11 gggtsg 16
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ilarity 100.0%;
Conservative (
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99US-0121825

99US-0123548

99US-0125788

99US-0126785

99US-0126785

99US-0128714

99US-0128714

99US-0128714

99US-0130449

99US-0130510

99US-0132048

99US-0132048

99US-0132486

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99US-0134768

99US-0135124

99US-0135124

99US-0135124

99US-0135124

99US-0135782

99US-0135782

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99US-0162142.
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Pred. No. 4.4e+02;
Mismatches 0;
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03-AUG-1999
04-AUG-1999
05-AUG-1999
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06-AUG-1999
09-AUG-1999
11-AUG-1999
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25-AUG-1999
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27-AUG

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99US-0147204
99US-0147204
99US-0147300
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99US-0147416
99US-0147935
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99US-0151080
99US-0151080
99US-0151080
99US-0151080
99US-0151080
99US-0151303

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08-JUN-1999
10-JUN-1999
110-JUN-1999
110-JUN
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99US-013840.
99US-0139450.
99US-0139453.
99US-0139456.
99US-0139456.
99US-0139456.
99US-0139460.
99US-0139462.
99US-0139462.
99US-0139462.
99US-0139463.
99US-0139763.
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99US-0144086.
99US-0145088.
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RESULT 18
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AC AAG115
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promoter;
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RESULT 19
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                                                                Score 33; DB 21;
Pred. No. 4.4e+02;
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AAB94509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Matches 6; Conserv
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N-PSDB; AAZ11066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human heat shock protein homologue 1 (HSPHH-1) protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC
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                                                                                                                                  Human protein sequence SEQ ID NO:15218.
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75 gggtsg 80
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                                         primer; detection; diagnosis; antisense therapy; gene therapy.
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Pred. No. 5e+02;
; Mismatches 0;
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Human;

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                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                             CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc oligonucleotide sequences defined in the specification, where the cc onligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide which comprises a 5'-end cc of an oligonucleotide comprising a sequence complementary to the cc sequence and an oligonucleotide comprising a sequence complementary to a combination of complementary to the comprises a 5'-end cc oligonucleotide which comprises a 5'-end sequence, where the cc oligonucleotide comprises a 3'-end sequence, where the cc oligonucleotide comprises a 1'-end sequence, where the cc in gene therapy. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, and classification and/or diagnosis of the abnormality of the proteins encoded by comparison and comparison of the abnormality of the proteins encoded by comparison to an analysis of the primers allow obtaining of the full-length cC comparison thuman cDNAs equences; AAB92446 to AAB13633 to AAB13642 represent human acid sequences; AAB92446 to AAB13632 cr the full-length class, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
       Human secreted protein bp537_4
                                        18-JAN-1999
                                                                     AAW69428
                                                                                              AAW69428 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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27-AUG-1999;
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, Sugiyama
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                                                                                                                                                                                                                                                                                                        348 AA;
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                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 99JP-0248036.
; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                              Protein; 378
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T, Wakama
                                                                                                                                                                                                                                           100.0%;
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Pred. No.
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A, Nagai K,
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                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                                             Protein identification; signal transduction pathway; metabolic pathway;
                                   Arabidopsis thaliana
                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                       AAG12987;
                                                                                                                                                                                             AAG12987 standard; Protein; 499
                                                            termination
                                                                                                                                            17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 24; Page 79-80; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotides and secreted proteins - useful as, e.g. nutritional additives, immunostimulators, haemotopoiesis regulators and as diagnostic agents
                                                                         ybridisation assay;
                                                                                                                                                                                                                                                                252 gggtsg
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11-MAR-1997;
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                                                            sequence
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97US-0815381
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                                                                    mapping; gene expression control; promoter;
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Pred. No. 5.4e+02;
0; Mismatches 0;
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RESULT 23
AAC48191
ID AAC48191;
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Best Local
Matches
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05-MAR-1999;
09-MAR-1999;
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24-SEP-1999
28-SEP-1999
29-SEP-1999
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07-OCT-1999
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14-OCT-1999
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12-OCT-1999
12-OCT-1999
21-OCT-1999
                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                 25-FEB-2000;
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                                                                                                                                               Arabidopsis thaliana.
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6; Conserv
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ilarity 100.0%;
Conservative (
                                                               2000EP-0301439
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        99US-0121825.
99US-0123180.
99US-0123548.
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99US-0156458
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99US-0157753
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                                                                                                                                                                                                                               protein fragment
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                                                                                                                                                                                                                              SEQ
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. 6.9e+02;
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  23-MAR-1999
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Best Local
Matches
                                               29-JUL-199;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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10-OCT-1999
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WPI; 2001-318749/34.
                                                                                          28-JUL-2000;
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                                                                                                                                                Human;
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             ß
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             Isogai T,
, Sugiyama'
                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
6; Conservative
                                  HELIX
                                                                                                                                                                                                        standard;
                                               99JP-0248036.
99JP-0300253.
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2000JP-0241899.
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                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy.
             Nishikawa
T, Wakama
                                                                                                                                                                                                        Protein;
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             Wakamatsu
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                                                                                                                                                                                                        520
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                      'n,
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Pred. No.
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                    Hayashi K,
             Nagai K,
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                    Saito
              Otsuki
                                                                                                                                                                                                                                                                                    Length 499;
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              Η.
                    Yamamoto J;
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16-JUL-1999
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9905-0156658.
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RESULT
AAG1298
ID AA
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Best Loc
Matches
    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
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   99US-0121825.
99US-0123548.
99US-0125788.
99US-01267864.
99US-0126786.
99US-0127462.
99US-0128234.
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99US-0131449
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netic mapping; gene expression control; promoter;
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Pred. No. 7.5
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                              Primer sets for synthesizing polynucleotides, particularly tfull-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
                                                                                                                             Ota T,
Ishii
                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                 07-FEB-2001
                                              Claim
                                                                                                                                                        (HELI-)
                                                                                                                                                                          09-JUN-2000;
                                                                                                                                                                                                                               28-JUL-2000;
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                       Human;
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                                                                                                                                                                                                                                                                                                                                                                              AAB94160 standard; Protein; 557
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Sugiyama
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2000JP-0241899.
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ilarity 100.0%;
Conservative
                                              ID 14452;
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T, Wakamatsu
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A, Nagai F
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent cligonucleotides, all of which are used in the exemplification of the present invention.
              AAH52304 to AAH53970 represent nucleic acids (I) encoding polyp (II), given in AA681454 to AA683120, from Staphylococcus epider (I) and (II) can have antibacterial acity try and therefore can in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which exp
                                                                                                                                                                 Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 5602 nucleotide sequences defin oligonucleotide comprises at least of an oligonucleotide comprising a
                                                                                                                                     Claim 18;
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                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
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DB; AAH52843.
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                                                                                                                                 Page 315; 2188pp; English.
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                                                                                                                                                                   polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 22;
Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                polypeptides epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the 5'-end
               express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                  the
                                                                  be used
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the
be
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polypeptides (II) (and/or nucleic acids) may

then

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AAM40004
ID AAM
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Best Local
Matches
                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; gene therapy; cancer; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; archemotactic; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing only goes up to SEQ ID NO.4454 so even though sequences are given in the disclosure for SEQ ID NO.4454 to 4472, no sequences are present for SEQ ID NO.4455 to 4461.
                                                                                                                                                             Tang
Wang
Zhao
                                    Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
    Example 4; SEQ
                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 3149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM40004 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 gggtsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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                                                                                                2001-442253/47.
DB; AAI59160.
                                                                                                                                                         Wang Z,
Zhou P,
                                                                                                                                                                                                                                       HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US34263
    Ð
                                                                                                                                                     Asundi V, Chen R,
Wehrman T, Xu C,
Goodrich R, Drma:
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 602
3149; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 22; I
Pred. No. 7.9e+02;
Pred. No. 7.9e+02;
                                                                                                                                                       nen R, Ma Y,
lu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
                                                                                                                                                                     Qian )
Yang
                                                          for
                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 582;
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                                                                                                                                                                       Ren F,
Zhang
                                                        disorders
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                                                                                                                                                                                           Wang
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RESULT
AAM4 0003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAAJ8642-AAAJ2213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC claised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed CC specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                          21-JAN-2000;
25-APR-2000;
09-JUL-2000;
            WPI; 2001-442253/47.
N-PSDB; AAI59159.
                                                 Zhao
                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                        14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                  19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              chemokinetic; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM40003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM40003 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                   leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGTSG
||||||
83 gggtsg
                                             g YT, Liu C,
g J, Wang Z,
o QA, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602
                                                                                                                                      2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                            2000US-0727344
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                                             Asundi V, Ch
Wehrman T, )
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO
                                                            Chen R,
Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                         3148
                                                                                                                                                                                                                                                                                                                                                           drug screening; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
Pred. No.
                                                Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                            Ma
Xue
                                            e AJ,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 8.1e+02; thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВB
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                                                            g xB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                           Ren F,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                            ŗ,
                                                                       Wang
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RESULT :
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38462-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                            09-JUN-2000;
                                                                                                                                                                                                                            11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                     EP1074617-A2
                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                             27-AUG-1999;
                                                                                                                                                                                                                                                                               29-JUL-1999;
                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB94603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB94603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggtsg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders.
                                                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
6; Conser
                                                                                                                        Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625
                                                                                                                                                                                                        99JP-0300253
2000JP-0118776
2000JP-0183767
2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence SEQ ID NO:15428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã,
                                                                                                                                                                                                                                                                             99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
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                                                                                                                    Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 678 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3148; 10078pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                  Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                  Saito K, y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 625;
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                                                                                                                                   Yamamoto
          detection by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Claim 8;

SEQ ID 15428; 2537pp + CD ROM; English

Ashbya gossypii nucleotide and protein fungal growth inhibitors

sequences useful for identifying

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
""tches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc sequence and an oligonucleotide which comprises a 5'-end cc polynucleotide which comprises a 3'-end sequence complementary to a composition of comprises a 3'-end sequence, where the combination of composition of comprises at least 15 nucleotides and the combination of the 5'-end sequence, and sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the cc detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13638 and Cc AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to cc AAB95893 represent human amino acid sequences; AAB92446 to cc AAB95893 represent human amino acid sequences; AAB92446 to cc of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                 (NOVS)
                                                                                                                                                                                                                                                                                                                                                                    phosphatidylinositol-4 kinase; cytokenesis gene; fungal fungicidal; filamentous fungi; plant pathogen; Septoria Stagnospora nodorum; Magnaporthe grisea; human pathogen; Candida albicans; Aspergillus fumigatus.
                                                              WPI; 2000-317988/27
N-PSDB; AAA14503.
                                                                                                               Gaffney
                                                                                                                                                                                                                                   06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-binding protein; AG003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY84686 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-ord primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                   08-OCT-1998;
                                                                                                                                                                                                                                                                   20-APR-2000
                                                                                                                                                                                                                                                                                                     WO200022133-A1
                                                                                                                                                                                                                                                                                                                                      Ashbya gossypii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of AG003, a GTPase activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY84686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                             NOVARTIS AG.
NOVARTIS-ERFINDUNGEN VERW GES
                                                                                                             TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678
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                                                                                                               Wendland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                   99WO-EP07501
                                                                                                               Ċ,
                                                                                                             Dietrich F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2071
                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPase activating protein; fungal growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 22
Pred. No. 9e+02;
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                                                                                                         Philippsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.
                                                                                                                                                                                                                                                                                                                                                                                                    s; fungal development;
Septoria tritici;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 678;
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Best Local S
Matches 6
This invention describes a novel polynucleotide isolated from human immunodeficiency virus type I subtype C/B', which can be used for the induction of specific humoral and the immune responses. (I) and polypeptides (II) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevent of human immune deficiency virus-1 (HIV-1) infections, also for ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with fungicidal activity can be used for suppressing fungal growth, especially of filamentous fungi. Fungi that can be suppressed incluplant pathogens (e.g. Septoria tritici, Stagnospora nodorum, and Magnaporthe grisea) and human pathogens (e.g. Candida albicans, and Aspergillus fumigatus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding protein genes, recomposition of the protein gene, and a putative cytokenesis gene. These genes are protein gene, and a putative cytokenesis gene. These genes are essential for fungal growth and development. The proteins can be used in methods to identify compounds that have fungicidal activity. Compounds in methods to identify compounds that have fungicidal activity. Compounds in methods to identify compounds that have fungicidal activity.
                                                                                                 Disclosure;
                                                                                                                                    New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection;
cellular in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB86196 standard; Protein; 3025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         designated AG003. The specification also describes putative G binding protein genes, putative phosphatidylinositol-4 kinase
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                                                                                                                                                                                 WPI; 2001-336417/36.
                                                                                                                                                                                                          Wagner
                                                                                                                                                                                                                                                                               16-NOV-1999;
                                                                                                                                                                                                                                                                                                         16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                    31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus
                                                                                                                                                                                                                                    SHAO Y. GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1mmune
                                                                                                                                                                                                         Wolf H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
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                                                                                                 8A-0;
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response;
                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                            Shao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                              48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human;
                                                                                                                                                                                                                                                                                                                                                                                                    Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; treatment;
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                                                                                                 German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; antiviral;
reatment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                       a stop codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4e+03;
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  prevention
or rational
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Query Match Best Local Matches

Similarity 5; Conserv

Conservative

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Mismatches

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Score 30; Pred. No.

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32

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Match

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RESULT 34
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Best Local
                                    of a phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. M4.
The encoding pdh nucleic acid is used to produce recombinant Rhodococcus L-phenylalanine dehydrogenase, which can be used to produce L-mino acids from the corresponding alpha-keto acids, e.g. to produce L-phenylalanine from phenylpyruvic acid (e.g. for the production of aspartame), to screen for phenylketonuria in newborn infants and to monitor the efficacy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111111
2639 gggtsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in
                                                                                                                                                                              DNA encoding Rhodococcus L-phenylalanine production of recombinant enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. stearothermophilus alanine dehydrogenase fragment #1
Sequence
                                                                                                                                                                                                                          WPI; 1999-080406/07
                                                                                                                                                                                                                                                                                                          05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                    05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
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                                                                                                                                                   Disclosure; Fig 4; 30pp; English.
                                                                                                                                                                                                                                                   Blanchard
                                                                                                                                                                                                                                                                              (YESH
                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phenylalanine
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                           low-phenylalanine diets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method
                                                                                                          sequence is used to describe a method which results in the isolation phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. M4.
                                                                                                                                                                                                                                                                              ) UNIV YESHIVA EINSTEIN COLLEGE
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6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                               production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase; pdh; L-amino acid; phenylpyruvic acid;
duction; phenylketonuria; infant; alanine dehydrogenase;
                                                                                                                                                                                                                                                                                                          95US-0461990
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pathway; promoter;

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RESULT
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     Matches
                                  Query Match
                                                                                         This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
                                                                         Sequence
                                                                                                                                                                                                                                                                                            Claim 11; Page 228; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                      respiratory tract and central nervous
                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences from Staphylococcus aureus wCHU29 useful in vaccines and for treatment of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-252940/23.
N-PSDB; AAV53319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT,
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       Local Similarity hes 5; Conserv
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       Conservative
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represented as Xaa in the specification"
                 90.9%;
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, Pratt JM,
  Score 30; DB Pred. No. 3.4e
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RW,
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11-MAY-1999
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05-MAR-1999

09-MAR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          termination
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RESULT 37 AAG15635

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Best Local S
Matches
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26-OCT-1999;
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                                                                                                  Similarity 83.: 5; Conservative
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              (first entry)
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
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                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence; corn.
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25-FEB-2000; 06-SEP-2000. EP1033405-A2

2000EP-0301439

99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788.

lea mays subsp.

mays.

17-OCT-2000

(first entry)

ID

NO:

31888

pathway; promoter;

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Query Match
Best Local Similarity bo...
Thes 5; Conservative
                                                                                                                                                                                                                   This sequence is used to describe a method which results in the isolation of a phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. M4. The encoding pdh nucleic acid is used to produce recombinant Rhodococcus L-phenylalanine dehydrogenase, which can be used to produce L-mino acids from the corresponding alpha-keto acids, e.g. to produce L-phenylalanine from phenylpyruvic acid (e.g. for the production of aspartame), to screen for phenylaketonuria in newborn infants and to monitor the efficacy of low-phenylalanine diets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phenylalanine dehydrogenase; pdh; L-amino acid; phenylpyruvic acid; aspartame production; phenylketonuria; infant; alanine dehydrogenase; diet.
                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt DNA} encoding Rhodococcus L-phenylalanine dehydrogenase -production of recombinant enzyme
                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-080406/07
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9905-0142 9905-0142 9905-0143 9905-0143		0-0	0-5	0-S	0-5	0-S	- S	S-0	0-5 0-5	-S 0-S	-S 0S	-S 0-S	<u> </u>	- S - O - S	0-S 0-S	0-20 0-20	S-0	0-2 0-2 0-2	- S	S-0	S-0	0.0	S-0	0-0	20.0	- S	īs-0	0-S	-0 -0	0-20	0.00
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42977. 42977. 43542. 43624.	055 390 803	287 842 154	823 991	354 695	353 353	763 817	463 750	461	459 460	457 458	455	492	452	540 847	724 094	528 502	782	021	124 353	768 941	370	219	256	487	405	407	449 048	510 891	449	077 077	234
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Matches 5; Conservative
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P33531
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lycopersico
caenorhabdi
secherichia
4 saccharomyc
2 homo sapien
7 escherichia
4 salmonella
4 salmonella
5 brachydanio
4 streptomyce
5 streptomyce
5 rattus norv
                                                                                                                                                                                                                                                       7 homo sapien
1 rattus norv
5 homo sapien
3 human cytom
3 dictyostell
7 caenorhabdi
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K1CJ_MOUSE
K1CJ_HUMAN
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YQI6_CAEEL
K2C1_MOUSE
HS72_MOUSE
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YA83_MYCPN
ZIC2_HUMAN
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DLD2_BACSU
LORI_MOUSE
Y136_TREPA
CDSN_HUMAN
GATC_DROME
USP_DROME
CEA1_SHISO
                                                                                                                                                                                                                                                                                                                                                       DHSU_CHRVI
HXB3_MOUSE
COAA_BPIKE
SOX3_HUMAN
CAH9_HUMAN
RBL2_CHRVI
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HM10_CAEEL
JUNB_MOUSE
JUNB_RAT
MURG_AQUAE
Y217_AQUAE
MURG_HELPY
YM79_YEAST
MURG_ENTHR
MURG_BORBUJ
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UVRA_THEMA
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YA68_MYCTU
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treponema p mycobacteri saccharomyc

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ALIGNMENTS

musculu

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YNI2_METTL
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RESULT 2
CDX4_HUMAN
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Matches 6
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15-JUL-1998
30-MAY-2000
                                                                      "Genomic structure of the human CDX4 gene: a present of the FG syndrome.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                          Chen E.Y., States D.J.,
Submitted (MAY-1997) to
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Chen E.Y., States
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDX4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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MEDLINE-88259240; PubMed-2838639;

Souillard N., Magot M., Possot O., Sibold L.;

"Nucleotide sequence of regions homologous to nif

protein) from the nitrogen-fixing archaebacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL PROTEIN IN NIFH2 3'REGION (FRAGM
                               <del>: :</del>
                                                                                                                                                                  Chiaroni P., Colleaux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  014627;
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NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR: S00739; SUU/35.
InterPro; IPR000205; NAD_binding.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of regions homologous to nifH (nitrogenase protein) from the nitrogen-fixing archaebacteria Methanococcus thermolithotrophicus and Methanobacterium ivanovii; evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2186;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 implications."
J. Mol. Evol.
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                             SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
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S00739; S00739.
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6; Conserv
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C PROTEIN CI
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. 36, Last sequence update)
. 39, Last annotation update)
CDX-4 (CAUDAL-TYPE HOMEOBOX
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                                                                                                                                                                    L.,
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the EMBL/GenBank/DDBJ
                        he EMBL/GenBank/DDBJ databases.
NUCLEAR (BY SIMILARITY).
O THE CAUDAL FAMILY OF HOMEOBOX PROTEINS
                                                                                                                                                                    Briault S.,
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                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; | Catarrhini; Hominidae;
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Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Rosales; Rosaceae.
                                                                                                                                                                                                                                                                                                                                                                  MDL1_PRUDU STANDARD; PRT; 559 AA. 024243; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
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PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00031; HTHREPRESSR.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02835; MIM; 300025;
                                                                                                                                                                                                                          Suelves M.;
                                                                                                                                                                                                                                       STRAIN-CV.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRUDU
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PROSITE: PS50071: HOMEOBOX_2: 1.
Homeobox: DNA-binding: Developmental protein: Nuclear protein:
                                                                                          +++
                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                 NCBI_TaxID=3755;
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InterPro; IPR000047;
InterPro; IPR001356;
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                                                                      SIMILARITY).

CATALYTIC ACTIVITY: MANDELONITRILE - CYANIDE + BENZALD COFACTOR: FAD (BY SIMILARITY).

SUBUNIT: MONOMER (BY SIMILARITY).

SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                             mitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: INVOLVED IN CYANGENIS, THE RELEASE OF HCN FROM INJURED TISSUES, CATALYSES THE STEEREOSPECIFIC ADDITION OF HCN TO A VARIETY OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN (BY
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AF029879;
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AAD01894.1;
AAD01894.1;
AAD01894.1;
                                                                                                                                                                                                                                       TISSUE-Flower;
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dons; core eudicots; Rosidae;
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TISSUE-seed;
Wu H.-C., Poulton J.E.;
Wu H.-C., Poulton J.E.;
"Immunocytochemical localization of mandelonitrile black cherry (Prunus serotina Ehrh.) seeds.";
Plant Physiol. 96:1329-1337(1991).
-!- FUNCTION: INVOLVED IN CYANOGENIS, THE RELEASE (TISSUES. CATALYSES THE STEREOSPECIFIC ADDITION
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NCBI_TaxID=23207;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
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TE; PS00623; GMC_OXRED_1;
TE; PS00624; GMC_OXRED_2;
Glycoprotein; FAD; Flavo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y08211; CAA69388.1;
                                                                                                                                                                                 Poulton J.E.;
ted (DEC-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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DNA of Prunus
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(R)-MANDELONITRILE LYASE ISOFORM FAD (ADP PART) (PROBABLE).
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EMBL: U78814; AAB38536.1; -.
InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
                                                                                                                                                               P23531;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIBC-LAC) (LACTOSE-PERMEASE IIBC COMPONENT)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-LAC).
            MEDLINE-91093107; pubMed-2125052; de Vos W.M., Boerrigter I.J., van Hengstenberg W.; "Characterization of the lactose-
                                                                                                                                                                                                                                                                LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00623; GMC_OXRED_1; PROSITE; PS00624; GMC_OXRED_2;
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STRAIN-MG1820;
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 phosphotransferase
                                                                                                                   Bacteria; Firmicutes;
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DEVELOPMENTAL STAGE: ABSENT FROM UNTIL 6 WEEKS AFTER FLOWERING. THE DEVELOPMENT, THE LEVEL OF ENZYME
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SIMILARITY: BELONGS TO
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N-LINKED (GLCNAC. . . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL);
152367E736AF5FDD CRC64;
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); Mismatches
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                                   Rooyen
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                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIBC-LAC)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II,
(EC 2.7.1.69) (EII-LAC).
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                                    Bacteria; Firmicutes;
                                                 Streptococcus
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P50976;
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InterPro: IPR003501; PTS_IIB.
Pfam; PF02378; PTS_EIIC; 1.
Pfam; PF02302; PTS_IIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphotransferase system; Sugar
Phosphorylation; Transmembrane; F
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Pred. No. 1.1e+02;
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1.1e+02; DB 1;

Length 568

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J. Gen. Microbiol. 139:2685-2694(1993).

-I- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSPEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSEY E.L., Stewart G.C.;

"Nucleotide and deduced amino acid sequences of the lack, lacABCD and lacFE genes encoding the repressor, tagatose 6-phosphate gene cluster, and sugar-specific phosphotransferase system components the lactose operon of Streptococcus mutans.";

J. Bacteriol. 174:6159-6170(1992).
                                                                                                                                                                                                                         Phosphorylation;
DOMAIN 1
      SEQUENCE
                                                                                                                                                                                                                                                                     Pfam; PF02302; PTS_IIB; 1.
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InterPro; IPR003352; PTS_EIIC.
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MEDLINE-94103744; PubMed-8277252;
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STRAIN-UA130 / SE
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SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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PF02378; PTS_EIIC; 1.
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A129FDD14282EAAE CRC64;
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P24400;
01-MAR-1992
01-MAR-1992
01-FEB-1995
PTS SYSTEM,
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J. Biol.
-!- FUNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (
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InterPro; IPR003352; PTS_EIIC.
InterPro; IPR003501; PTS_IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breidt F. Jr., Hengstenberg W., Finkeldei U., Stewart G.C.; "Identification of the genes for the lactose-specific components the phosphotransferase system in the lac operon of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-88059023; PubMed-2824493;
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NCBI_TaxID=1280;
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01-JUL-1989
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FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANFERACE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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Firmicutes; Bacillus/Clostridium gro
Firmicutes; Bacillus/Clostridium gro
Firmicutes; Bacillus/Clostridium gro
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LACTOSE-SPECIFIC IIBC COMF
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COMPONENT (EIIBC-LAC) (LACTOSE-
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BC COMPONENT)
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Best Local :
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"Molecular cloning and DNA sequence of lacE, the gene encoding the lactose-specific enzyme II of the phosphotransferase system of Lactobacillus casei. Evidence that a cysteine residue is essential for sugar phosphorylation.";

J. Biol. Chem. 265:22561-22568 (1990).

J. BIOL. THIS IS A COMPONEUT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE PRIMARY
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RESULT . 9
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RESULT 1
GCKR_RAT
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007071;
01-OCT-1994
01-FEB-1995
30-MAY-2000
GLUCOKINASE
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014397; 099522;
01-NOV-1997 (Rel. 35, Cr
30-MAY-2000 (Rel. 39, La
20-AUG-2001 (Rel. 40, La
GLUCOKINASE REGULATORY F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayward B.E., Dunlop N., Intody S., Lee Hayward B.E., Bonthron D.T.;
"Organization of the human glucokinase Genomics 49:137-142(1998).
-!- FUNCTION: INHIBITS GLUCOKINASE BY E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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ProDom; PD025295; GCKR; 1.
PROSITE; PS01272; GCKR; 1.
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MEDLINE-98334554; PubMed-9570959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAEDLINE=96014291; PubMed=8589523; Warkham A.F., Bonthron D.T.; Warner J.P., Leek J.P., Intody S., Markham A.F., Bonthron D.T.; "Human glucokinase regulatory protein (GCKR): cDNA and genomic cloning, complete primary structure, and chromosomal localization."; Mamm. Genome 6:532-536(1995).
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Mammalia; Eutheria;
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MEDLINE-96014291; PubM
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InterPro; IPR001347; SIS.
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SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY
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                       (Rel. 30, Greated)
(Rel. 31, Last sequence update)
(Rel. 39, Last annotation update)
REGULATORY PROTEIN (GLUCOKINASE R
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/FTId=VAR_008906.
DE750462AC603C80 CRC64;
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Pred. No. 1.2e+02;
; Mismatches 0;
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Catarrhini;
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                         REGULATOR).
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AC P12035;
DT 01-OCT-1989
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Matches 6
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InterPro; IPR001741; GCKR.
InterPro; IPR001347; SIS.
Pfam; PF01380; SIS; 1.
ProDom; PF025295; GCKR; 1.
PR0SITE; PS01272; GCKR; 1.
               SEQUENCE FROM N.A.
MEDLINE-87254239; PubMed-2439698;
Klinge E.M., Sylvestre Y.R., Free-
"Evolution of keratin genes: diff-
different pathways.";
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                                                                                                                                                             Homo sapiens (Human, Fukaryota; Metazoa;
                                                                                                                                                                                                            KRT3.
                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KERATIN, TYPE II CYTOSKELETAL 3 (CYTOKERATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                    Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequencing of rat liver cDNAs encoding the regulatory protein of glucokinase.";
FEBS Lett. 339:312-312(1994).
-!- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS
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TISSUE-Liver;
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Detheux M., Vandel
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Mammalia; Eutheria; Rodentia;
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SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
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321:111-115(1993).
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Primates;
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                                     Freedberg I.M., Blumenberg different protein domains
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Catarrhini;
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Pred. No. 1.2e+02;
Mismatches 0;
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RI Nat. Genet. 16:184-187(1997).

C I SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.

C II SUBUNIT: HETEROTETRAMER OF TWO TYPE II KERATINS.

C II SUBUNIT: HETEROTETRAMER OF TWO TYPE II KERATINS.

C INTISSUE SPECIFICITY: CORNEA-SPECIFIC.

C INTERIOR CORNEAL DYSTANDIA DATA DE SEASE THAT CAUSES FRAGILITY OF THE COLOR.

C INTERIOR CORNEAL EPITHELIUM. PATIENTS ARE USUALLY ASYMPTOMATIC UNTIL ADULTHOOD WHEN RUPTURE OF THE CORNEAL MICROCYSTS MAY CAUSE CONTROL AND INTERMITTENT DIMINUTION OF VISUAL ACUITY.

CC EROSIONS, PRODUCING CLINICAL SYMPTOMS SUCH AS PHOTOPHOBIA, CONTACT LENS INTOLERANCE AND INTERMITTENT DIMINUTION OF VISUAL ACUITY.

CC RARELY, SUBEPITHELIAL SCARRING CAUSES IRREGULAR CORNEAL ACUITY.

CC RARELY, SUBEPITHELIAL SCARRING CAUSES IRREGULAR CORNEAL CONTROL ASTIGMATION SHOWS A DISORGANIZED AND THICKENED EPITHELIUM WHITH CC EXAMINATION SHOWS A DISORGANIZED AND THICKENED EPITHELIUM WHITH CC DEBRIS-LADEN INTRAEPITHELIAL CYSTS.

CC INDICATE THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILIAR KERATIN: I (ACIDIC; 40-55 KDA) [K9 TO KZO] AND II CRC (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K8]

CC (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

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CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]

CO (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K2]
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Best Local Similarity
Matches 6; Conserv
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DOMAIN
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InterPro; IPR003054; Keratin_II.
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"Mutations in cornea-specific keratin K3 or K12 genes cause"
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intermediate
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148043; -.
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/FIIG-VAR 003668.
22748619A828BCD9 CRC64;
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Pred. No. 1.2e+02;
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STRAIN-AX3;
MEDLINE-94229358;
                                                                Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
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SPORE COAT PROTEIN SP87 PRECUR
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                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                        P54643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betaherpesvirinae; Cytomegalovirus.

NCBI_TaxID=10360;
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-I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL32, EHV-1 28, EBV BFLF1, HCMV UL52, AND VZV 26.
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PIR; S09815; QOBEW1.
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Dev. Biol. 163:49-65(1994).
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InterPro; IPR001628; zf-C4.
Pfam; PF00105; zf-C4; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-48
                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z79604; CAB01900.1;
HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Tr
Zinc-finger.
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|- FUNCTION: ORPHAN NUCLEAR RECEPTOR.

|- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

|- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE
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Similarity 100.0%;
6; Conservative (
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120
160
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C4-TYPE.
C4-TYPE.
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Pred. No. 1.5e+02;
  Craniata; Vertebrata; Euteleostomi;
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01-JUL-1993 (Rel. 2
01-FEB-1996 (Rel. 3
ATP-DEPENDENT CLP F
                                                                                                        CLAB_LYCES P31542;
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CONFLICT
SEQUENCE
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between
      Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                             CD4B.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ223599; CAA11465.1; -. EMBL; AF083330; AAC33291.1; -. InterPro; IPR001752; kinesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muresan V., Abramson T., Lyass A., Winter D., Porre
Chamberlin N.L., Schnapp B.J.;
"KIF3C and KIF3A form a novel neuronal heteromeric
                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99023472; PubMed=9808286; Faire K., Gruber D., Bulinski J.C.; "Identification of kinesin-like molecules in myogenic cells."; Eur. J. Cell Biol. 77:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associates with membrane vesicles.";
Mol. Biol. Cell 9:637-652(1998).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                 1 GGGTSG
                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES.
SUBJUNT: HETERODIMER OF KIF3A AND KIF3C.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II SUBFAMILY.
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PR00380; KINESINHEAVY.
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                                                                                                                                                                                                                                                                                                                                                                         Microtubules;
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                            KINESIN_MOTOR_DOMAIN1; 1.

crotubules; ATP-binding; Coiled coil; Neurone.

377

ECHANCHEMICAL (MOTOR) (BY SIMILARITY).

632

COLLED COIL (POTENTIAL).
                                                           26, Created)
26, Last sequence update)
33, Last annotation updat
PROTEASE ATP-BINDING SUBU
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Solanales; Solanaceae;
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POLY-GLY.
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Pred. No.
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                                                          update)
3 SUBUNIT CLPA HOMOLOG CD4B
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core eudice; Solanum
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RESULT 17
CLAA_LYCES
   Matches
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Best Local
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01-JUL-1993
01-JUL-1993
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Lycopersicon esculentum (Tomato).

Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core et

Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solar
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NP_BIND
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease in prokaryotes and eukaryotes.";
Proc. Natl. Acad. Sci. U.S.A. 87:3513-3517(1990).
-!- FUNCTION: MAY INTERACT WITH A CLPP-LIKE PROTEASE INVOLVED DEGRADATION OF DENATURED PROTEINS IN THE CHLOROPLAST.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                  ATP-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gottesman S., Squires C., Pichersky E., Carrington M., Mattick J.S., Dalrymple B., Kuramitsu H., Shiroza T., Clark W.P., Ross B., Squires C.L., Maurizi M.R.; "Conservation of the regulatory subunit for the Clp AN
MEDLINE=90239044; PubMed=2185473;
              SEQUENCE FROM N.A.
                                           NCBI_TaxID=4081;
                                                                                                                                    PRECURSOR.
                                                                                                                                                                                                                           CLAA_LYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00300;
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InterPro; IPR001270;
InterPro; IPR001943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=90239044; PubMed=2185473;
                                                                                                                                                                                                                                                                                                   244 GGGTSG
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Milarity 100.
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Proc. Natl. Acad. Sci. U.S.A. 87:3513-3517(1990).

-I- FUNCTION: MAY INTERACT WITH A CLPP-LIKE PROTEASE INVOLVED DECRADATION OF DENATURED PROTEINS IN THE CHLOROPLAST.
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STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden F
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.;
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                                                                                                                                                                         Jordan A., Aragall E., Gibert I., Barbe J.; Promoter identification and expression analysis of Salmonella typhimurium and Escherichia coli nrdEF operons encoding one of class I ribonucleotide reductases present in both bacteria."; Mol. Microbiol. 19:777-790(1996).
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STRAIN=K12;
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
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                        SEQUENCE FROM N.A
                                                 Science
                                                                        Gregor J., Davis N.W.,
Mau B., Shao Y.;
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     S_YEAST
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P47044;
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MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

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"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

1- FUNCTION: NOT KNOWN; PROBABLY INVOLVED IN RIBONUCLEOTIDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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Nature 409:529-533(2001).
[5]
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MEDLINE-21074935; PubMed-11206551;
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DNA Res. 4:91-113(1997).
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                                                                                                                                                 GGGTAG
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PF02555; NrdI; 1.
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33, Created)33, Last sequence up35, Last annotation
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83.38;
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Lagawa M., Makino K., Miki T., Mitsuhashi N.,
Nakade S., Nakamura Y., Nashimoto H.,
Saito N., Sampei G., Satoh Y., Sivasundaram S.
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; Pred. No. 87;
1; Mismatches
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RESULT 21

IF31_HUMAN STANDARD; PR
ID IF31_HUMAN STANDARD; PR
AC 075822;
DT 30.MAY-2000 (Rel. 39, Created)
DT 30.MAY-2000 (Rel. 39, Last seque
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Block K.L., Vornlocher H.-P., Hershey
"Characterization of cDNAs encoding the translation initiation factor e1F3.";
translation initiation factor e1F3.";
J. Biol. Chem. 273:31901-31908
                       EMBL; U97670;
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POhl T.M., Aljinovic G.;

Submitted (SEP-1995) to the EM

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Mammalia;
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Saccharomyces cerevisiae (Baker's yeast).
Succharomycet; Rungi; Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomyces
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NP_BIND 13 20
SEQUENCE 245 AA; 26
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FUNCTION: BINDS TO THE 40S RIBOSOME
METHIONYL-TRNAI AND MRNA.
SUBUNIT: EIF-3 IS COMPOSED OF AT LE/
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                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE-97426617; PubMed-9278503;
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30-MAY-2000
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STRAIN-ATCC 14028s;
MEDLINE-95173114; PubMed-7868611;
Stojllykovic I. Baeumler A.J., Heffron F.;
"Ethanolamine utilization in Salmonella typhi
"Ethanolamine utilization, and mutational
sequence, protein expression, and mutational
cohB eutE eutG eutH gene cluster.";
J. Bacteriol. 177:1357-1366(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-ATCC 14028S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOFOID E.C., Rappleye C.A., Stojiljkovic I., Roth J.R.; "The 17-gene ethanolamine (eut) operon of Salmonella tylencodes five homologues of carboxysome shell proteins." J. Bacteriol. 181:5317-5329(1999).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Actinopterygii; Neopterygii; Teleostei; Eute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETHANOLAMINE
                                                                        15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
HOMEOBOX PROTEIN OTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18560; AAA80210.1; -. EMBL; AF093749; AAC78119.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99395039; PubMed-10464203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=602;
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5; Conserv
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(Rel. 32, Last sequence update)
(Rel. 39, Last annotation updat
E UTILIZATION PROTEIN EUTJ.
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83.3%;
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Last annotation updat
(ZOTX3).
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1; Mismatches
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                                                                                             update
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typhimurium: nucleotide
analysis of the cc
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1.8e+02
     Vertebrata; |
Euteleostei;
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                        Euteleostom1;
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     Ostariophysi;
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MURG_STRCU
ID MURG_STRCU
ID MURG_STR
AC Q9X4H4;
DT 30-MAY-2
DT 30-MAY-2
DT 20-AUG-2
DE UDP-N-AC
DE PYROPHOS
DE (EC 2.4.)
DE TRANSFEF
GN MURG.
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                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                Transcripts during zebrafish embryogenesis;

Resin Res. Mol. Brain Res. 27:221-231(1994).

C -!- FUNCTION: MAY PLAY A ROLE IN VERY EARLY EMBRYOGENESIS,

GASTRULATION, AND THE DEVELOPMENT AND SUBDIVISION OF THE
DIENCEPHALON AND THE MIDBRAIN. MAY PLAY A ROLE IN THE ORGANIZER

C -!- SUDCELLULAR LOCATION: NUCLEAR (PROBABLE).

C -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

C -!- SUBCELLOHANT L STAGE: DETECTED ALONG THE MARGINAL ZONE OF SYMMETRIC

C -!- SUBCELLOHANT AND FOUND AT THE SYMMETRIC

C -!- SUBCELOPMENT, AT 5 HRS OF DEVELOPMENT AND FOUND IN THE DIENCEPHALON

STRIPES AT 5 HRS OF DEVELOPMENT AND FOUND IN THE DIENCEPHALON

STRIPES AT 18 HRS OF DEVELOPMENT, AND FOUND IN THE DIENCEPHALON

C -!- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
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HSSP; P06601; IPJL.
ZFIN; ZDB-GENE-980526-27; otx3.
InterPro; IPR001356; Homeobox.
InterPro; IPR003025; Otx_TF.
Pfam; PF00046; homeobox; 1.
                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLICLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
             (EC 2.4.1.-)
TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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PRINTS; PR01255; OTXHOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE~95206106; PubMed-7898305;
MORIH., Miyazaki Y., Morita T., Nitta H., Mishi
"Different spatio-temporal expressions of three
"Different spatio-temporal expressions of three
                                                                                                                                                                                                                        203
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162 F
36145 MW;
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POLY-SER.
POLY-SER.
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RESULT
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Best Local
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-AUG-2000 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
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Kuennen R.
Submitted
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SEQUENCE
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                                                                                                                          Rajandream M.A.;
                                                                                                                                           Saunders
                                                                                                                                                               STRAIN-A3(2);
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
Actinomycetales; Stre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 40733;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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             FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY
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                                                                                                                                           D.C.,
                                                                                                                                                                                     FROM
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362 AA; 38847 MW; OB
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                                                                                                                                           Harris
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83
                                                                                                                                         D., James
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...
OF PEPTIDOGLYCAN
                                                                                                                                                                                                                          er B.
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                                                                                                                                                                                                                        .T., McCormick J.R.;
EMBL/GenBank/DDBJ databases
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1; Mismatches
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                                                                                                                                       K.D.,
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                                                                                                                                       Parkhill
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0;
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                                                                                                databases
                                                                                                                                     J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell wall;
                                                                                                                                       Barrell B
                                                                                                                                                                                                                                                                                                                                                  Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
tent is in
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                                                    GLCNAC
(LIPID
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RESULT 27
MAF2_RAT
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Best Local Similarity
Thehes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane; Peptidoglycan synthesis SEQUENCE 364 AA; 38842 MW; D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U10879; AAD10537.1; -.
EMBL; AL109663; CAB51993.1; -.
Transferase; Glycosyltransferase; Cell division; Cell wall;
                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                              Sakai M., Imaki J., Yoshida K., C
Kuboki Y., Nishizawa M., Nishi S.
"Rat maf related genes: specific
                                                                                                                                                                                                                                                                                            STRAIN=WISTAR;
MEDLINE=97190228; PubMed=9038383;
MEDLINE=97190228; PubMed=9038383;
MEDLINE=97190228; PubMed=9038383;
                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAF2_RAT
                                                                                                                                EMBL; U56242; AAB50063.1;
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                  Oncogene 14:745-750(1997).
-I- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                     spinal cord. "
                                                                                                                                                                                                                                                                                                                                                                                                      MAF2 OR MAF
                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
                                                                            Nuclear
                                                                                     Proto-oncogene; Transcription
                                                                                               SMART; SM00338; BRLZ; 1.
                                                                                                           HSSP; P05412; 1JUN.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                        - I - SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P54844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE MURG FAMILY.
 protein.
139
169
180
191
212
225
4D 284
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173
187
187
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234
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 POLY-ALA.
POLY-HIS.
POLY-HIS.
POLY-GLY.
POLY-GLY.
BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; L
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                      regulation;
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                                                                                      DNA-binding; Activator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
                                                                                                                                                                                                                                                                                   chondrocytes, lens
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                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       Murinae;
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                                                                                                                                                                                                                                                                                                                                                                       Rattus
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MAF2_MO
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   Query Match
Best Local
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P54843;
01-OCT-1996
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                                             DNA_BIND
DOMAIN
SEQUENCE
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   Similarity
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90.

Score Pred.

30;

DB 1; 2.3e+02;

Length 370

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SQ
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HSSP; P05412; 1JUN.
TRANSFAC: T01432; -
MGD; MGI:96909; Maf.
InterPro; IRR001871; bzIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression.";
Mol. Cell. Biol. 15:246-254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kurschner C., Morgan J.I.;
"The maf proto-oncogene stimulates transcription from multiple sites
in a promoter that directs Purkinje neuron-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C; TISSUE-Cerebellum; MEDLINE-95097997; PubMed-7799931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE C-MAF INTERACTION SITE WAS MAPPED TO THE SEQUENCE 5'-[GT]GG]N[GT]NCTCAGNN-3' IN THE L7 PROMOTER. IT MAY INTERACT WITH ADDITIONAL BASIC-ZIPPER PROTEINS THAT DETERMINE A SUBTYPE OF MAF-RESPONSIVE ELEMENT BINDING.
SUBUNIT: HOMO- OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.9%;
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MW.
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Pred. No.
                                                                                                                                              POLY-HIS.
POLY-HIS.
POLY-SER.
POLY-GLY.
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288E464708DA6C7D CRC64;
LEUCINE-ZIPPER.
76A9517EFF9C777C
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                                                                         BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                 POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                              regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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    CRC64;
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RESULT 29
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Matches 5
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P17557;

O1-AUG-1990 (Rel. 15, Created)

O1-AUG-1990 (Rel. 15, Last sequence update)

O1-OCT-1994 (Rel. 30, Last annotation update)

E ALANINE DEHYDROGENASE (EC 1.4.1.1).

Bactlius stearothermophilus.

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bactlius/Staphylococcus group; Geobacillus.
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                                                                                                                                                                                                                                                                              ACT_SITE
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000598; AlaDh_PNT.
InterPro; IPR000205; NAD_binding.
Pfam; PF01262; AlaDh_PNT; 1.
PROSITE; PS00836; ALADH_PNT_1; 1.
PROSITE; PS00837; ALADH_PNT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M33299; AAA22211.1; -. PIR; B34261; B34261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuroda S., Tanizawa K., Sakamoto Y., Tanaka H., Soda K. "Alanine dehydrogenases from two Bacillus species with thermostabilities: molecular cloning, DNA and protein s determination, and structural comparison with other NAD(P)(+)-dependent dehydrogenases.", Biochemistry 29:1009-1015(1990).

-i- FUNCTION: THIS ENZYME IS A KEY FACTOR IN THE ASSIMI L-ALANINE AS AN ENERGY SOURCE THROUGH THE TRICARBOX CYCLE DURING SPORULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
STRAIN-IFO 12550;
                                                                 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90254112; PubMed=2340274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLAULAR LOCATION: CYTOPLASMIC.

MISCELLANEOUS: THE B.STEAROTHERMOPHILUS ENZYME RETAINED ABOUT 50
MISCELLANEOUS: THE B.STEAROPHILUS ENZYME RETAINED ABOUT 50
OF ITS INITIAL ACTIVITY WHEN HEATED BT 85 DEGREES CELSIUS FOR 5
MIN AT PH 7.2, WHEREAS THE B.SPHABRICUS ENZYME LOST THE SAME
ACTIVITY WHEN HEATED AT ONLY 65 DEGREES CELSIUS FOR 5 MIN.
SIMILARITY: STRONG, TO OTHER ALANINE DEHYDROGENASES AND PARTIAL
WITH PYRIDINE NUCLEOTIDE TRANSHYDROGENASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMOHEXAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC
                                                                 GGGTAG
                                                                                                          GGGTSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTSG
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                                                                                                                                                            Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                        PS00836; ALADH_PNT_1; 1. PS00837; ALADH_PNT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                   170
372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + NADH.
                                                               180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVITY: L-ALANINE + H(2)O + NAD(+) =
                                                                                                                                                                                                                                                                                <u>}</u>
                                                                                                                                                                                                                                                                                                  96
200
                                                                                                                                                                                                                                                                              39694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND PARTIAL SEQUENCE
                                                                                                                                                                           90.9%;
                                                                                                                                                                                                                                                                                                                                                  Sporulation.
                                                                                                                                                                                                                                                                 POTENTIAL.
NAD (BY SIMILARITY).
, 99AE8E621ED1F23A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                              Score 30; [
Pred. No. 2.
                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                             ,в
..3e+02;
0;
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                                                                                                                                                                                                       --
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                                                                                                                                                                                               Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soda K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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AC 004650
DT 01-JUN
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                                                                                             Query Match
Best Local
                                                                         Matches
                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                             SEQUENCE
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1 GGGTSG
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Pfam; PF00045; homeobox; 1.
Pfam; PF00412; LIM; 2.
ProDom; PD00094; LIM; 2.
SMART; SM00389; HOX: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
01-JUN-1994
30-MAY-2000
                                                                                                                                                                                                                                                                                                     SMART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
PROSITE; PS00478; LIM_DOMAIN_1;
PROSITE; PS50023; LIM_DOMAIN_2;
PROSITE; PS00027; HOMEOBOX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German M.S., Wang J., Chadwick R.B., Rutter W.J.;

"Synergistic activation of the insulin gene by a LIM-homeo domain protein and a basic helix-loop-helix protein: building a functional insulin minienhancer complex.";

Genes Dev. 6:2165-2176(1992).

-I-FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR BY BINDING TO THE FLAT ELEMENT WHICH IS A BETA-CELL-SPECIFIC TRANSCRIPTIONAL ENHANCER FOUND IN THE RAT INSULIN GENE AND INTERACTING THROUGH ITS LIM-CONTAINING AMINO TERMINUS WITH SH-PAN, A HELIX-LOOP-HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T01958; -. InterPro; IPR001356; InterPro; IPR001781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X81406; CAA57163.1; .. PIR; B46233; B46233.
                                                                                                                                                                                                                                    Transcription
                                                                                                                                                                                                                                                             LIM domain;
                                                                                                                                                                                                                                                                             domeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93051335; PubMed=1358758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMX1A OR LMX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIM/HOMEOBOX PROTEIN LMX1A (LMX-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMXA_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "ISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM SUBFAMILY.
SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P02836;
       Similarity
5; Conserv
                                                                                                                   35 85

36 147

195 254

257 265

382 AA; 42802
       Conservative
                                                                                                                                                                                                                                                        Repeat; Metal-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 29, Created)
(Rel. 29, Last seq
(Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1HDD.
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                            90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homeobox
                                                                                                                                                                                                                                                                           Developmental protein;
                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
annotation update)
(LMX-1) (LIM-HOMEOBOX PROTEIN 1).
                          Score 30; DB 1;
Pred. No. 2.4e+02;
                                                                                                                                                                                       LIM 1.
LIM 2.
                                                                                                                 POLY-GLN.
2675E6F298EE9486 CRC64;
                                                                                                                                                                 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                             Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ⋛
                                                                                                                                                                                                                                                                         Nuclear protein;
                                                Length 382;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
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Gaps
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277 GGGTAG

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SERC_YEAST
ID SERC_YEAST
AC P333330;
                                                                               RESULT
 Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                EMBL; L20917; AAA20886.1; -.
EMBL; U19714; AAA85703.1; -.
EMBL; Z75092; CAA99393.1; -.
PIR; S42680; S42680.
HSSP; P23721; IBUN.
SWISS-2DPAGE; P33330; YEAST.
YEPD; 5420; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT).
SER1 OR SERC OR YOR184W.
                                                                             BINDING
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes B., Pohl T.M.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ

-I- CATALYTIC ACTIVITY: O-PHOSPHO-L-SERINE + 2

3-PHOSPHONOOXYPYRUVATE + L-GLUTAMATE.

-I- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    significant homology to t
aminotransferase.";
Yeast 10:385-389(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belhumeur P., Fortin N., Clark M.W.;
Belhumeur P., Fortin N., Clark M.W.;
"A gene from Saccharomyces cerevisiae which codes for a significant homology to the bacterial 3-phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Melcher K., Kuenzler M.,
Submitted (JAN-1995) to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                      pfam; pF00266; aminotran_5; 1.
proDom; pD001544; Phosphser_amintransf; 1.
pROSITE; pS00595; AA_TRANSFER_CLASS_5; 1.
Serine blosynthesis; Transferase; Aminotral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-94287715; PubMed-8017107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                               Pyridoxal phosphate.
BINDING 218 2
                                                                                                                                                                                                     InterPro; IPR000192; Aminotransf_class_V.
InterPro; IPR003248; Phosphser_amintransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: REQUIRED BOTH IN MAJOR PHOSPHORYLATED PATHWAY OF SERINI BIOSYNTHESIS AND IN THE BIOSYNTHESIS OF PYRIDOXINE. SUBUNIT: HOMODIMER (BY SIMILARITY). SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMINOTRANSFERASES
                                                                                                                                                                                                                                     ; 5420; -.
$0005710; SER1.
   Similarity
5; Conserv
                                                                                395 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                               218
                                                                                43415
                 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braus G., Entian K.D.;
the EMBL/GenBank/DDBJ d
                                                                                ¥
    Score 30; DB
Pred. No. 2.5e
1; Mismatches
                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FD -> LH (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                A22F020CC969B4BC
                                                                                                                                            Aminotransferase;
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лв
..5e+02;
0;
                                 DB 1;
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2 OXOGLUTARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                Length 395
                                                                               CRC64;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein with
    0,
      Gaps
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DDL_TREPA STANDARD; PRT; 396 AA.

AD SER: 1998 (Rel. 37, Last sequence update)

DT 15-DE-1998 (Rel. 37, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-ALA-D-ALA LIGASE; Last sequence update)

DT 20-ALA-D-ALA LIGASE; Last sequence update)

DE CD-LAR-D-ALA LIGASE; Last sequence update)

DE CD-LAR-D-ALA LIGASE; Last sequence update updates up
MURG_MYCLE
ID MURG_MYCLE
AC 069552;
DT 30-MAY-2000
DT 30-MAY-2000
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                                                                                                                                    RESULT
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Best Local
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006224;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE-N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSPHORYL-UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
                         Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                 TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       MURG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL022602; CAA18668.1;
EMBL; AL583920; CAC31295.1;
Leproma; ML0914; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Glycosyltransferase; Cell division; Cell wall; Peptidoglycan synthesis; Complete proteome.

SEQUENCE 407 AA; 42422 MW; B757B73C092C53F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
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UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
PYROPHOSYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
(EC 2.4.1..) (UNDECAPRENYL-PP-MURNAG-PENTAPEPTIDE-UDPGLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFERASE
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                                                                                          OR MT2212 OR MTCY270.15
   Corynebacterineae;
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Mycobacteriaceae;
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Mycobacterium
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I.
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I.
Cole S.T., Brosch R., Parkhill J., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
A Oliver S., Seeger K., Skelton S., Squares S., Squares R.,
Brutter S., Seeger K., Skelton S., Squares S., Squares R.,
A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
A Complete genome sequence.*;
The Complete genome sequence.*;
Nature 393:337-544(1998).
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Best Local
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YA68_MYCTU STANDARD; PRT; 4
95416;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2001 (Rel. 39, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
"HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV
RV1068C OR MT1097 OR MTV017.21C.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        Bacteria; Firmicutes;
Actinomycetales; Cory
                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist; Rv2153c; -.
Transferase; Glycosyltransferase; Cell division; Cell wall;
Peptidoglycan synthesis; Complete proteome.
SEQUENCE 410 AA; 41860 MW; 96902AFE356FC30B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE007068; AAK46496.1; -. TIGR; MT2212; -.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-!- FUNCTION: CELL WALL FORMATION. CATALYZES T
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SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MURG FAMILY.
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                                              Actinobacteria;
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Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                     463
                                 Actinobacteridae;
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2.6e+02;
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MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. RA Gordon S.V., Elglmeker K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the RT complete genome sequence.";

L Nature 393:537-544(1998).
    RESULT
MDL3_PF
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01-OCT-1996 (Rel. 34, Last
15-DEC-1998 (Rel. 37, Last
(R)-MANDELONITRILE LYASE I
(HYDROXYNITRILE LYASE 3) (
                                                                             LPRUSE
MDL3_PRUSE
P52707;
                                                                                                                                                                                                                                                                                                                                                          Hypothetical CONFLICT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL021897; CAA17184.1; EMBL; AE006991; AAK45353.1; TIGR; MT1097; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-:- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CDC 1551 / Oshkosh
Fleischmann R.D., Alland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-CDC 1551 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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InterPro; IPR000084; PE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
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PD001223; PE; 1.
protein; Complete
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E LYASE ISOFORM 3 PRECURSO
YASE 3) ((R)-OXYNITRILASE
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CF5696A7E9593952 CRC64;
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-> S (IN REF. 2).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene."; Plant Physiol. 115:1359-1397).

-1- FUNCTION: INVOLVED IN CYANOGENIS, THE RELEASE OF HCN FROM INJURED TISSUES. CATALYSES THE STERROSPECIFIC ADDITION OF HCN TO A VARIED.
                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00623; GMC_OXRED_1; 1. PROSITE; PS00624; GMC_OXRED_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U51562; AAA96782.1; -. EMBL; AF013161; AAB67714.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prunus serotina (Black cherry).
Eukaryota; Viridiplantae; Streptophyta; Embryc
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Rosales; Rosaceae; Prunus.
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00732;
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Hu Z., Poulton J.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000172; GMC_oxred
                                                                                                                                                                                                                                                                                                                                                                                                                                      lyase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                         1 GGGTSG
||||:|
60 GGGTAG
                                                                                           60
                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUES. CATALYSES THE STEREOSPECIFIC ADDITION OF HOW TO A VARIETY OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN.

CATALYTIC ACTIVITY: MANDELONITRILE - CYANIDE + BENZALDEHYDE.

COFACTOR: FAD.

SUBCELLULAR LOCATION: PRIMARILY FOUND WITHIN PROTEIN BODIES OF THE COTYLEDONARY PARENCHYMA CELLS WITH LESSER AMOUNTS WITHIN THE PROCAMBIUM (BY SIMILARITY).

SIMILARITY: BELLORS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                              Similarity 83.3
5; Conservative
                                                                                                                                                                                                             28
55
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145
162
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                           STANDARD;
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30
75
145
1150
1162
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252
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257
267
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309
400
420
420
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427
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27
573
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                                                                                                                                                          90.9%;
                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                     Flavoprotein;
                                                                                                                                            Score 30; DB Pred. No. 3.5e 1; Mismatches
                                                                                                                                                                                                         FAD (ADP PART) (PROBABLE

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                             (R)-MANDELONITRILE LYASE
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                          DB 1;
3.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
                           ξ
                                                                                                                                                                                                                                                                                                                                                                                               (PROBABLE)
                                                                                                                                                                       Length 573;
                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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NP_BIND
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MULZ.
Prunus serotina (Black cherry).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Commercial Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                              EMBL; AF040078; AAB96763.1; -. EMBL; AF040079; AAB96764.1; -. InterPro; IPR000172; GMC_oxred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eurosids I; Rosales; Rosaceae; NCBI_TaxID=23207;
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15-DEC-1998 (Rel. 3
(R)-MANDELONITRILE
 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILTED (JAN-1998) to the EMBL/GenBank/DDBJ databases. FROM INJURED FUNCTION: INVOLVED IN CYANOCENIS, THE RELEASE OF FLON TO A VARIETY STRUCTION OF HCN TO A VARIETY OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN (BY
           GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROCAMBIUM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: PR
COTYLEDONARY PARENCHYMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).

SIMILARITY).

CATALYTIC ACTIVITY: MANDELONITRILE - CYANIDE + BENZALDEHYDE COFACTOR: FAD.
GGGTAG
                                                                                                                                                                                                                                                                                                                       PF00732; GMC_oxred; 1.
TE; PS00623; GMC_oxrED_1;
                                           Similarity 5; Conser
                                                                                                                                                                                                                                                                                                               PS00624; GMC_OXRED
                                                                                                 576
66
                     δ
                                           Conservative
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56
31
47
76
146
151
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37,
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                                                   300
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ISOFORM 2 PRECURSOR (EC 4.1.2.10)
((R)-OXYNITRILASE 2).
                                                                                                 ₹.
                                                                                                                                                                                                                                                                                                   Flavoprotein;
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                                                                                             N-LINKED (GLCNAC.
                                       Score 30; DB Pred. No. 3.6e 1; Mismatches
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N-LINKED (GLCNA
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                                                    .6e+02;
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                                                            Length 576;
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RESULT 38

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RESULT 39
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                                                                                                                                                                                                                                                                                                                       SMART; SM00028;
                                                                                                                                                                                                                                                                                                                                                     EMBL; AB018262; BAA34439.1; HSSP; P53041; 1A17.
                                                                                                                                                                                                                                                                                                                                                                                                            modified
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                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                               Pfam; PF00515; TPR; 10
                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                              1 GGGTSG
||||:|
25 GGGTAG
                                                                25
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR THAT ACCELERATES THE IMPORT OF ALL MITOCHONDRIAL PRECURSOR PROTEINS (BY SIMILARITY).

SUBBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AN ILBAST 8 DIFFERENT PROTEINS (BY SIMILARITY).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL OUTER MEMBRANE (BY SIMILARITY).

SIMILARITY: CONTAINS 10 TPR REPEATS.
                                                                                                        Similarity
5; Conserv
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PRECURSOR PROTEINS IMPORT RECEPTOR (TRANSLOCASE OF OUTER
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           STANDARD;
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           PRT;
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Catarrhini;
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RA Kuehl P. Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Right M., Rodriguez I., Sakamoto N.,
RA Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.";
Rating Alon, Raff-Convoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., King B., King B., Kochiwa H., King B., Kochiwa H., King B., Kochiwa H., King B., King B., Kochiwa H., King B., King B., Kochiwa H., King B., King B., Kochiwa H., King B., King B., Kochiwa H., King B., King B
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-I- FUNCTION: RECEPTOR THAT ACCELERATES THE IMPORT OF ALL

-I- SUBUNIT: RECEPTOR THAT ACCELERATES THE IMPORT OF ALL

-I- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF

LEAST 8 DIFFERENT PROTEINS (BY SIMILARITY).
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Arakawa T.,
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Mammalia; Eutheria;
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SMART; SM00028; TPR; 10.
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                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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Rel. 40, Last sequence update)
Rel. 40, Last annotation update)
PRECURSOR PROTEINS IMPORT RECEPTOR (TRANSLOCASE OF OUTER
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                                                                                                                                                                                                                                                                                                          POTENTIAL
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Conno H., Adachi J.,
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Fukuda S.,
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"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

I Nature 399:323-329(1999).

I Nature 399:323-329(1999).

I NATURE STHE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS COMPANYING THE MODIFIED BASE(S). UVRA IS AN ATPASE STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

I SUBCULTLAR LOCATION: CTYOPLASMIC (BY SIMILARITY).

I SUBCELLLIAR LOCATION: CTYOPLASMIC (BY STAILARITY).

I SUBCELLIAR LOCATION: CONTAINS TWO ABC DOMAINS.
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Matches 5; Conservative
                                                                                                                                        Matches
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Best Local
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Q9WYVO;
30-MAY-2000
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SEQUENCE
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STRAID-MSB8 / DSW 3109;

STRAID-99287316; PubMed*10360571;

MEDLINE*99287316; Pub
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Bacteria; Thermotog
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TIGR; TM0480; -.
InterPro; IPR003439; ABC_transportr.
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-binding; Zinc-finger; Complete proteome.
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BIND 617 624 ATP (POTENTIAL)
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Search completed: February 4, 2002, 08:01:10
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4 rhynchosteg 3 platyhypnid 7 homo sapien

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Q9dw22 rat cytomeg
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Q9nzt0 homo sapien
Q9np55 homo sapien
Q9vp10 drosophila
O62416 caenorhabdi
O80450 arabidopsis
Q91yp4 arabidopsis
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Q9KNU2
Q9SA43
O9c753 arabidopsis
O9gu27 diabrotica
O9knu2 vibrio chol
O9sa43 arabidopsis
O9a9h8 caulobacter
O9xi68 arabidopsis
O9a4m5 caulobacter
O9xi69 arabidopsis
O9a607 caulobacter
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O9nwd0 homo sapien
O9cbv6 mycobacteri
O914h3 brevibacter
O9xh2 toxoplasma
O9eus5 streptomyce
O9mlw9 arabidopsis
O35028 bacillus su
O9nwm3 homo sapien
O9zdj4 erwinia chr
O9xd4 staphylococ
O9s3n3 bacillus ce
O9vn86 drosophila
O9jzq0 neisseria m
O9jut5 drosophila
O9n67 drosophila
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P84865 lactobacill
O996v0 neurospora
O9sinl arabidopsis
O56765 human cytom
O9asr6 arabidopsis
O9by4 mus musculu
O9bj1l caenorhabdi
O9v195 drosophila
O9v196 drosophila
O17368 caenorhabdi
O9v161 drosophila
O17366 caenorhabdi
O9sdc5 oryza sativ
O17476 ashbya goss
O19v64 homo sapien
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Q27403 drosophila
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Q9w0n5 drosophila
Q9w0n5 drosophila
Q82435 prunus sero
Q9fj97 arabidopsis
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Q99s77 staphylococ
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Q9DW22;
Q1-MAR-2001
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STRAIN-COLUMBIA;
MEDLINE-99087489; Pu
Nakamura Y., Sato S
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Tabata S.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K22F20.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                  SEQUENCE FROM N.A.
STRAIN-MAASTRICHT;
MEDLINE-96357047; PubMed-8764031;
Vink.C., Beuken E., Bruggeman C.A.;
"Structure of the rat cytomegalovirus
J. Virol. 70:5221-5229(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,013,767 bp covered physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
EMBL; AB016873; BAB10357.1; -.
SEQUENCE 218 AA; 22937 MW; C8551D884AB1FFD5 CRC64;
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Viruses; dsDNA viruses, no RNA stage; H
Betaherpesvirinae; Muromegalovirus.
   STRAIN-MAASTRICHT;
MEDLINE-20366325;
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S., Asamizu E.,
     PubMed=10906222,
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"Transformation of Piromyces communis xylanase to submitted (AUG-2000) to the EMBL/GenBank/DDBJ data EMBL; AF297649; AAG18439.1; -

InterPro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLHYDRLASE11.

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NON_TER

SEQUENCE 224 AA; 24976 MW; 93E512C9DF176DDE CI
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O9HFT3;
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XYLANASE (FRAGMENT).
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Eukaryota; Fungi; Ch
Neocallimasticaceae;
                                                                    Streptococcus gordonii Bacteria; Firmicutes;
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6; Conservative
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e DNA sequence of the rat c
74:7656-7665(2000).
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                   (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence up
(TrEMBLrel. 17, Last annotation
SFERASE LACE (FRAGMENT).
                                                                                                                                                                                                                                                                                   212
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                                                                       Bacillus/Clostridium group; Streptococcaceae;
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Best Local
Matches
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                   Q9NP55
Q9NP55
Q9NP55;
Q9NP55;
Q1-QCT-2000 (TremBLrel. 15, Created)
Q1-QCT-2000 (TremBLrel. 15, Last sequence update)
Q1-QCT-2001 (TremBLrel. 17, Last sequence update)
Q1-QUN-2001 (TremBLrel. 17, Last annotation update)
LUNX PROTEIN (NASOPHARYNGEAL CARCINOMA-RELATED PROTEIN) (TRACHEAL EPITHELIUM ENRICHED PROTEIN) (BA49G10.5) (LUNX PROTEIN (LOC51297)).
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01-OCT-2000
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Strains.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210773; AAG39000.1;
InterPro; IPR003501; PTS_IIB.
Pfam; PF02302; PTS_IIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 256 AA; 26710....
                                                                 TISSUE-LUNG;
                                                                                               SEQUENCE FROM
                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLUNC
Homo sapiens (Human).
Homo sapiens (Human).
'arvota; Metazoa; Chordata;
'horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NZTO;
                                Watanabe
                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                               Homo sapiens (Human)
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gene specifically expressed
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                                                                                                                                                                                       Primates;
                                                                                                                                                                                                                 Chordata;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB Pred. No. 1.5); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB
Pred. No. 1.5
); Mismatches
                                                                                                                                                                             Catarrhini; Hominidae;
                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandarl D., Bolshakov S.,
RA Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew E., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VYL0
Q9VYL0;
01-MAY-2000 (TrEN
01-MAY-2000 (TrEN
01-JUN-2001 (TrEN
CG11085 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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Biochim. Biophys. Acta
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Liu W.D., Zhou W., Wang L.,
"cloning a new gene related
Submitted (JUN-1999) to the
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the human plunc gene, a gene product with nasopharyngeal restricted expression pattern. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11018263
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EMBL/GenBank/DDBJ databases.
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Fleischmann
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le R.F.,
วก S.N.,
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                    K.A.,
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RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Shownkeen
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Smith T.,
RA Shue B.C., Siden-Klamos I., Smith J.,
RA Shue B.C., Siden K., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodbage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodbage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT Shence 287:2185-2195(200).
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Best Local S
Matches 6
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01-AUG-1998 (TrEMBLrel. 0
01-JAN-1999 (TrEMBLrel. 0
Y22F5A, 5 PROTEIN.
Y22F5A,5
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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PRINTS; PRO0024; HOMEOBOX.
SMART; SM00389; HOX; 1.
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InterPro; IFR002952; Eggshell.
InterPro; IFR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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-!- SIMILARITY: TO OTHER HOMEOBOX
EMBL; AE003489; AAF48182.1; -.
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Submitted
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Similarity 100.0%;
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Pred. No. 1.7e+02;
; Mismatches 0;
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080450;

01-NOV-1998 (TrEMBLrel. 08

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O1-JUN-2001 (TrEMBLREL. 1
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Best Local :
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ROUNSLEY S.D., Kaul S., Lin X., Ketchum K.A., Cr
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Cr
Brandon R.C., Sykes S.M., Mason T.M., Kerlavage
Brandon R.C., Sykes S.M., Mason T.M., Kerlavage
Bomerville C.R., Venter J.C.;

"Arabidopsis thallana chromosome II BAC F16M14 g
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ da
EMBL; AC003028; AAC27174 1;

InterPro; IPR001005; Myb_DNA_bind.

PROSITE; PS50090; MYB_3; 1.
                                                                                                                            Q9LYP4;
Q9LYP4;
Q1-OCT-2000
01-OCT-2000
01-JUN-2001
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elegans.
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EMBL; AL021479; CAA163
SEQUENCE 279 AA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bevan M., Murphy G.,
Rudd S., Lemcke K., I
Submitted (APR-2000)
                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                   NCBI_TaxID=3702;
                                                                                                         T28J14_160.
                                                                                                                     HYPOTHETICAL
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                                SEQUENCE FROM N.A.
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ilarity 100.
Conservative
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AA; 30291 M
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AA; 34307
., Ridley P.,
Mayer K.F.X.
)) to the EMBL
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ntae: Streptophyta; Embryophyta; Tracheophyta;
liophyta; eudicotyledons; core eudicots; Rosid
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17,
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Pred. No. 1.7
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Best Local :
                                         075953;
01-NOV-1998 (TremBLrel. 08, 01-NOV-1998 (TremBLrel. 08, 01-JUN-2001 (TremBLrel. 17, HEAT SHOCK PROTEIN HSP40-3.
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InterPro: IPR003130; GED.
InterPro: IPR00626; Ubiquitin.
Pfem: PF02179; BAG; 1.
SMART; SM00264; BAG; 1.
SMART; SM00302; GED; 1.
SMART; SM00302; GED; 1.
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SEQUENCE
HOMO sapiens (Human).
Homo sapiens (Human).
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-!- SIMILARITY: TO RN
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
REVERSE TRANSCRIPTASE-LIKE PROTEIN (FRAGMENT).
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Eukaryota; Metazoa; Arthropoda; Chelicerata;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
SUBMBL; AL163652; CAB87278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-directed DNA polymerase
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SEQUENCE FROM N.A.
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Pred. No. 1.9e+02;
Mismatches 0;
      Craniata;
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C ACTIVE SITE (BY SIMULARITY).

C -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2:

C -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-

C -1- SUBUNIT: B CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-

C -1- SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

C -1- SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

C -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).

C -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.

REMBL, AF233567; AAG27527.1; -

REMBL, AF233567; AAG27527.1; -

REMBL; AF233567; AAG
                                                                                                                                                                                                                                                                                                 Inferred from Cladistic Augusters:

Data Sets: trnL-F, rps4, and rbcL.";

Bryologist 103:242-256(2000).

-1- FUNCTION: RUBISCO CARALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRACKENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Luna E., Buck W.R., Akiyama H., Arikawa T., Tsubota H., Gonzalez D., Newton A.E., Shaw A.J., Gonzalez D.; "Ordinal Phylogeny within the Hypnobryalean Pleurocarpous Inferred from Cladistic Analyses of Three Chloroplast DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen M.S., Laszlo A., Roti Roti J.I "Differential response of members stress agents in mammalian cells.", Submitted (SEP-1998) to the EMBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bryopsida; Bryidae; NCBI_TaxID=94508;
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Bryopsida;
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InterPro; IPR001623;
Pfam; PF00226; DnaJ;
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DnaJ_N.
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Pred. No.
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SEQUENCE
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Pfam; PF00016; RuBisCO_large; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Phylogeny of Selaginellaceae: evaluation of generic/subgeneric relationships based on rbcL gene sequences.";
Int. J. Plant Sci. 160:585-594(1999).
-I- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT) (FRAGMENT).
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    003112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) - PHOSPHO-GLYCERATE + 2-PHOSPHOGLYCOLATE - SUBBUAT: 8 LARGE CHAIMS + B SMALL CHAIMS (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korall P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopodiophyta;
Selaginella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3
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llarity 100.0%;
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    PRELIMINARY;
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Isoetopsida; Selaginellales; Selaginellaceae;
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Pred. No. 2.8e+02;
; Mismatches 0;
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01-JUL-1997 (TrEMBLrel. 04, Created)

01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4
                                                                                                                        Q31681 PRELIMINARY; PRT; 451 AA.
Q31681;
Q1-NOV-1996 (TrEMBLrel. O1, Created)
Q1-NOV-1996 (TrEMBLrel. O1, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4)
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ACT_SITE
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                                                       Eukaryota; Viridiplantae; Streptophyta; Andreaeopsida; Andreaeales; Andreaeaceae
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NCBI_TaxID=3207;
                                                                                      Chloroplast
                                                                                               Andreaea rupestris
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  "Phylogenetic analysis
Mol. Phylogenet. Evol.
                    Manhart J.R.;
                              MEDLINE-94356259;
                                       SEQUENCE FROM
                                                                                                                   LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                         392
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                                                                                                                                                                                                                                            1 GGGTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is L.A., Mishler B.D., Vilgalys R.;
Phylogenet, Evol. 0:0-0(1997).
FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
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 Phylogenet.
                                                                                                                   SUBUNIT) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                              449
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191
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                                       N.A.
                                                                                                                                                                                                                                                                                                              AA ;
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                               PubMed-8075831;
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191
449
                                                                                                                                                                                                                                                                                                              49596
                                                                                                                                                                                                                                                                       100.0%;
  of green plant rbcL 3:114-127(1994).
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                                                                    Andreaeaceae;
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Pred. No. 2.9
); Mismatches
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Photosynthesis.
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hes 0;
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                                                                             Embryophyta;
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                                                                     Andreaea
           sequences.";
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ACTIVATES
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                                                                                                                                                                                                                                                                                  Length
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                                                                             Bryophyta
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PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chloroplast; Lyase; Mono Oxidoreductase; Photorespiration; Photosynthesis.
                                                                                                                                                                                                   Chloroplast.
                                                                                                                                                                                                                                                           "Molecular phylogeny of brown algal genera Akkesiphycus (Laminariales), resulting in the circumscription of the Akkesiphycaceae and Halosiphonaceae."; Phycologia 39:416-428(2000).
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SETO INLAND SEAS;
Kewai H., Sasaki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Desmarestiaceae; D
NCBI_TaxID=114257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLYEL 17, Last annotation update)
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; stramenopiles; Phaeophyceae; Desmarestiales;
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                                                                                                                                                                                SEQUENCE
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CAPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2
PHOSPHO-D-GLYCERATE.

CAPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
GGGTSG
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451 AA;
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ilarity 100.0%;
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Pred. No. 3e+
D; Mismatches
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Pred. No. 2.9
); Mismatches
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OF CO(2)
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. 2.9e+02;
0;
                                                                                   3e+02;
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                                                                                                             DB 8;
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Best Local
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Q9H1J0;
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NON_TER
SEQUENCE
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Kew Bull. 55:257-309(2000).

-:- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF

-:- FUNCTION: SUBISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                       01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                        Pfam: PF00016; RuBisCO_large; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chioroplast; Lyase; Mono Oxidoreductase; Photorespiration; Photosynthesis
                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE RUBISCO EMBL; AJ402954; CAC04312.1; -. InterPro: IPR000685; RuBisCO_large.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cameron K.M., Johnson S.A., Lledo M.E
Sheahan M.C., Soltis D.E., Soltis P.S
Wurdack K.J., Chase M.W.,
"Phylogeny of the eudicots: a nearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=124965;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Icacinaceae; Gomphandra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4
                                   Homo
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00016; RuBisCO_large;
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                                                                                                                                                                                                 1 GGGTSG
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SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REACTIONS OCCUR SIMULTANEOUSLY AND ACTIVE SITE (BY SIMILARITY).
                                                                                                                                                                        GGGTSG
                                   sapiens (Human)
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6; Conser
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                                                           (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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ilarity 100.0%;
Conservative (
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51914
           Primates;
                       Chordata;
                                                         16,
16,
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.A., Lledo M.D.,
E., Soltis P.S.,
                                                                                                                                                                                                                                                                                       MW.
                                                           Created)
Last sequence
Last anno
                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                     Score 33;
Pred. No.
          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                             PRT;
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                                                         sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete familial analysis based
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                                                           update)
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Best Local S
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                                                                                                C PHOSPHO-D-GLYCERATE.

C -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-C

C PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCLATE.

C PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCLATE.

C -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.

R INTERPROPOSES: RubisCO_large.

R INTERPROPOSES: RubisCO_large.

PFAM; PF00016; RubisCO_large: 1.

R PFAM; PF00015; RUBISCO_LARGE; 1.

PGAM: PF00015; RUBISCO_LARGE; 1.

Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;

W Oxidoreductase; Photorespiration; Photosynthesis.

W Oxidoreductase; Photorespiration; Photosynthesis.

SEQUENCE 475 AA; 52740 MW; 4D7BA2D5CB15B7E7 CRC64;
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SEQUENCE FROM N.A.

PubMed=11163187;

Lykke-Andersen J., Shu M.-D., Steitz
f "Human Upf proteins target an mRNA f;

bound downstream of a termination co
t. Cell 103:1121-1131(2000).

REMBL: AY013251; AA048511.1; -.

470 AA; 56213 MW; C012
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Best Loc
Matches
                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-HIGASHI-HIROSHIMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Bryopsida;
                                                                                                                                                                                                                                                                                                                                                                                 Tsubota H., Nakao N., Arikawa
Deguchi H., Seki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bryopsida; Bryidae;
NCBI_TaxID=90343;
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Local :
                       1 GGGTSG
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                                              Similarity 6; Conserv
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6; Conserv
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                       o,
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                                             Conservative
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s target an mRNA fo
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Hypnales; Brachytheclaceae; Rhynchostegium.
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                                         Score 33; DB 8; 1
Pred. No. 3.1e+02;
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Pred. No.
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for nonsense-mediated
codon.";
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C ACTIVE SITE (BY SIMILIARITY).
C -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-
C PHOSPHO-D-GLYCERATE + C-PHOSPHOSLYCILATE:
C -1- SUBUNIT: B LARGE CHAINS + B SMALL CHAINS (BY SIMILARITY).
C -1- SUBUNIT: B LARGE CHAINS + B SMALL CHAINS (BY SIMILARITY).
C -1- SUBURIT: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
DE MBL; ABO29385; BAA86206.1: -
Interpro; IPRO00685; RUBISCO_LARGE.
PROSITE; PS00157; RUBISCO_LARGE; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
PROSITE; PS00157; RUBISCO_LARGE; Lyase; Monooxygenase;
W Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
W Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
W Oxidoreductase: Photorespiration; Photosynthesis.
SQ SEQUENCE 475 AA; 52740 MW; C3F5551355A19EEC CRC64;
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Best Local
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Q9BZI7;
Q1-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A preliminary phylogeny of Hypnales (Musci) as Inferred from chloroplast rbcl sequence data.";
Bryol Res. 7:233-248(1999).
-1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORSPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
SEQUENCE FROM N.A.
MEDLINE-20565755; PubMed-11113196;
Serin G., Gersappe A., Black J.D.,
"Identification and characterizatic
                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                           UPF3X.
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Q9TM63;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.
                                                                                                                                                                                                                                                                    UPF3X.
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Charvota; Viridiplantae;
                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                                                              Homo sapiens
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Deguchi H., Seki T.;
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Bryopsida; Bryidae;
NCBI_TaxID=98942;
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Metazoa; Chordata; C
~~+heria; Primates; (
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  A., Black J.D., Ard characterization
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                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pred. No.
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Aronoff R., Maquat L.E. on of human orthologues
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hes 0;
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                RA Ballew R.M., Basu A., AMI H.J., ANDEWS FRANKOCH C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhon G., Zhu X., Smith H.O.,
RA Shin Markin M. W., Moshin G.M., 
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Best Local :
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01-MAY-2000
01-JUN-2001
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MO1. Cell. Biol. 21:209-223(2001).
EMBL; AF318576; AAG60691.1; -
SEQUENCE 483 AA; 57762 MW; F5A8A395783D1A69 CRC64;
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Local Similarity 100.0%;
hes 6; Conservative
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Q9A4M2;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
Q9AA21 PRELIMINARY; PRT;
Q9AA21;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                         Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL: AE005946; AAK24772.1; -.
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PRINTS; PR00047; STRDHDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                             Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
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InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
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                                                                                                                                                                                                                                                                                                                                                                               Caulobacter
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87 GGGTSG
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                                                                                  GGGTSG
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Pred. No.
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Pred. No. 3.
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                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Caulobacter group;
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Best Loc
Matches
                                                                                 SEQUENCE FROM N.A.

MEDLINE-98022869; PubMed-9356176;
Bernardoni R., Vivancos V., Giang

glide/gcm is expressed and requi
Dev. Biol. 191:118-130(1997).
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01-NOV-1996
01-NOV-1996
01-JUN-2001
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Cell 82:1013-1023(1995).
[3]
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MEDLINE=960156097; PubMed=7553844;
HOSOYA T., Takizawa K., Nitta K.,

"glial cells missing: a binary swidetermination in Drosophila.";
Cell 82:1025-1036(1995).
                                                                                                                                                                                                                                                              Jones B.W., Fetter R.D., Tear G., "glial cells missing: a genetic so
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=96016096; PubMed=7553843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berr Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., W Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              027403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC0787.
Caulobacter
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13 GGGTSG
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OR GLIDE/GCM OR CG12245.
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6; Conserv
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Metazoa; Arthropoda; Tra
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nilarity 100.
Conservative
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ilidae; Drosophila
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EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     switch
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Mismatches 0;
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annotation update)
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            RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hilhards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botcher A., Dong Z., Mays A.D., Dav I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dinkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liang Y., Lin X.,
Liang Y., Lin X.,
Liang Y., Liang Y., Lin X.,
Liang Y., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., S
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Q9VLA5;
01-MAY-2000
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GCM PROTEIN.
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Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Dintera; Brachycera; Muso
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EMBL;
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InterPro; IPR003902; GCM_motif.
SeQUENCE 504 AA; 56168 MW;
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U34039; AAC46912.1;
U81164; AAC47808.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endopterygota; Dip
ilidae; Drosophila
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Pred. No. 3.3e+02;
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   RA Addms M.D., Celniker S.E., Holt R.A., Eyans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Hilt R.A., Eyans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Hilt R.A., Sabhurner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Diegvam C.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskenn D.R., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylers E., Spradling A.C., Srapteton M., Strong R.H., Wang X.Y., Wassarman D.A., Weinston M., Strong R.H., Wang X.Y., Wassarman D.A., Weinston G.M., Weissenbach J.,
RA Welson J., Shen M., Shupski M.P., Smith T.,
RA Sylers R.A., Weers E.M., Sunoria J., Ann W., Shang K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Hostin P., Shan M., Shaps W., Santh H.O.,
RA Jeng X.Y. Levit J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Hostin P., Shan M., Shan W., Shan M., Shan M
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Q9W0N5; PTEN
01-MAY-2000 (TrEN
01-MAY-2000 (TrEN
01-JUN-2000 (TrEN
CG13894
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Pterygota; Neoptera;
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NCBI_TaxID=7227;
[1]
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AE003625; AAF52790.1;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 14,
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Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0ED74C2D3B9BBCB0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.3e+02;
hes 0;
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Best Local
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Tabata S.;

*Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,013,767 bp covered physically assigned P1 and TAC clones.*;

DNA Res. 5:297-308(1998).
                                                               SEQUENCE FROM N.A. STRAIN-COLUMBIA; MEDLINE-99087489;
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01-NOV-1998
01-JUN-2001
                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                 01-MAR-2001 (TERMBLIEL 16, Create 01-MAR-2001 (TERMBLIEL 16, Last s 01-JUN-2001 (TERMBLIEL 17, Last a MANDELONITRILE LYASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                Hu Z., Poulton J.E.;
Submitted (MAR-1998) to the EMBL,
EMBL; AF053886; AAC61982.1; -.
Mendel; 33024; Pruse; 2903; 33024.
InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDL5.

Prunus serotina (Black cherry).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Eukaryota; Wadnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  082435
082435;
                                                          Nakamura
                                                                                                                                                                                                 Q9FJ97;
01-MAR-2001
                                                                                                                                                                                                                        Q9FJ97
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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NCBI_TaxID=23207;
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SEQUENCE 528 AA; 59427 MW;
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0V-1998 (TrEMBLrel. 08, Last sequence update)
UN-2001 (TrEMBLrel. 17, Last annotation update)
(+)-MANDELONITRILE LYASE ISOFORM MDL5 PRECURSOR.
                                                                                                                                                                                                                                                                                                                     6;
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6; Conserv
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PS00624;
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ilarity 100.
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                                                      PubMed=9872454;
S., Asamizu E.,
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GMC_OXRED_2;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                  Score 33; DB 10;
Pred. No. 3.7e+02;
; Mismatches 0;
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Pred.
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3.5e+02;
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                                                       Kotani
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                                                                                                                                eudicots;
                                                      Ξ.
                                                                                                                                         Tracheophyta;
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                                 5. VII.
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MEDLINE=21195684; PubMed=11296296;

Perretti J.J., McShan W.M., Ajdic D.J., Savic G. Perretti J.J., McShan W.M., Ajdic D.J., Savic G. Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Whi Yuan X., Clifton S.W., Roe B.A., McLaughlin R., "Complete genome sequence of an MI strain of Streptococcus Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; Ae006616; AAK34621.1; -.
Transferase; Complete proteome.

SEQUENCE 565 AA; 61209 MW; 122F40043FDA2D84 CRC64;
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
KUTOda M., Ohta T., Uchiyama I., Baba T., Yuzawa
Kuroda M., Ohta T., Uchiyama I., Nagai Y., Lian J.,
Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama
Matsumaru H., Maruyama A., Inoue R.I., Kaito C.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PTS SYSTEM, LACTOSE-SPECIFIC COMPONENT IIBC (EC
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SEQUENCE
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                                                                                                                                                 Q99877 PRELIMINARY; PRT; 570 AA.
Q99877;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.
NCBI_TaxID=1314;
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Bacteria; Firmicutes; Bacillus/Clostridium
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Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=158879;
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Loutes; Bacillus/Clostridium group;
Ylococcus group; Staphylococcus.
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Zhu H., Song L., White
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a A., Mizutani-Ui Y.,
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Submitted (JAN-1998) to the EMBL/G.
EMBL; AF053885; AAC61980.1; -
EMBL; AF053884; AAC61980.1; -
EMBL; AF043187; AAD02266.1; -
EMBL; AF043187; AAD02265.1; -
EMBL; AF043186; AAD02265.1; -
EMBL; AF043186; Pruse; 2903; 3350.
Mendel; 3350; Pruse; 2903; 35927.
Mendel; 35927; Pruse; 2903; 35927.
Mendel; 35928; Pruse; 2903; 35928.
InterPro; IFR000172; GMC_oxred.
PROSITE; PS00624; GMC_OXRED_2; 1.
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082784:
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; AP003136; BAB43282.1;
Complete proteome.
SEQUENCE 570 AA; 62414 MW
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Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant
aureus.";
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids 1; Rosales; Rosaceae; Prunus.
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Pred. No. 3.8e+02;
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01-OCT-2000 (TrEMBLE
01-JUN-2001 (TREMBLE
ORIGIN RECOGNITION C
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ database;
EMBL; AL353822; CAB86634.1; ...
Interpro; IPR001990; Granin.
PROSITE; PS00422; GRANINS_1; UNKNOWN_1.
SEQUENCE 578 AA; 63706 MW; E70100A0176F0FC4 CRC64;
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Eukaryota; Fungi; Ascomycot
Sordariales; Sordariaceae;
NCBI_TaxID=5141;
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Gosalbes M., Monedero V., Alpert C., Perez-Martinez G.;
"Establishing a model to study the regulation of the lactose
Lactobacillus casei.";
FEMS Microbiol. Lett. 148:83-89(1997).
EMBL; 280834; CAB02556.1;
InterPro; IPR00332; PTS_EIIC.
InterPro; IPR00332; PTS_IIB.
Pfam; PF02302; PTS_IIB; 1.
Pfam; PF02303; PTS_IIB; 1.
SEQUENCE 577 AA; 62367 MW; 32DB7B35E55607CB CRC64;
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STRAIN-ATCC 393 (PLZ15-);
MEDLINE-97218691; PubMed-
Gosalbes M., Monedero V.,
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(TrEMBLrel. 15, Last sequence update)
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GNITION COMPLEX SUBUNIT 2 RELATED PROT
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                                                                  PRELIMINARY;
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Pred. No. 3.8
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01-JUN-1998
01-JUN-2001
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               422 GGGTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10363;
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||||||
203 GGGTSG
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STRULING
STRAIN=TOWNE;

C STRAIN=TOWNE;

X MEDLINE=98241707; PubMed=9573236;

X Krosky P.M., Underwood M.R., Turk S.R., Feng K.W.-H., Jair Rrosky P.M., Underwood M.R., Turk S.R., Townsend L.B., Drain R.T., Townsend L.B., Drain Resistance of human cytomegalovirus to benzimidazole rib maps to two open reading frames: UL89 and UL56.*;

RI J. Virol. 72:4721-4728(1998).

RI J. Virol. 72:4721, AAC40816.1;

DR InterPro; IPR002597; Herpes_env.

DR InterPro; IPR002597; Herpes_env.

Pfam; PF01673; Herpes_env; 1.

SCO SEQUENCE 668 AA; 74154 MW; 049848D7A52596CC CRC64;
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RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Gronin L.A., Shen M., VenAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Cronin L.A., Shen M., VenAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creesy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;

RY Sequence and analysis of chromosome II of Arabidopsis thaliana.*;

RI "Sequence and analysis of chromosome II of Arabidopsis thaliana.*;

RMARI, ACO07087; AAN22995 1;

DR InterPro; IPR001440; TPR.

DR Pfam; PF00515; TPR; 6.

RMARI, SMO028; TPR; 4.

COCCURANCE SINGE SINGE COCKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytomegalovirus (strain Towne).
Viruses; dsDNA viruses, no RNA stage;
Betabherpesvirinae; Cytomegalovirus.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Last sequence update)
Last annotation updat
Score 33; DE
Pred. No. 4.5
); Mismatches
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Pred. No.
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, Drách J.C.;
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                         RC STRAIN-C57BL/GJ; TISSUE-LUNG;
RX MEDLINE-2108560; PubMed-11217851;
RX MEDLINE-2108560; PubMed-11217851;
RX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Okazaki Y., Gjosbori T., Bonol H., Kasukawa T., Sashio T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Matsushi H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Matsushi H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Matsushi H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Matsushi H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
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Best Local Similarity
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Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
"Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR367321; AAK32908.1;
"Submitted (MAR-2001) To the EMBL/GenBank/DDBJ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last support update)
01-JUN-2001 (TREMBLRel. 17, La
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR.; 8.
SMART; SM00082; LRRCT; 1.
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SMART; SM00369; LRR_TYP; 11.
SMART; SM00369; LRR_TYP; 11.
SEQUENCE 809 AA; 88809 MW;
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Q9BJL1;
Q1-JUN-2001
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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SEQUENCE
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Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;

Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;

"Caenorhabditis elegans nuclear receptor sequences exhibit biophysical comparability with the ligand-binding domain fold.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF332205; AAK17976.1; -.
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                                                                                                 This invention relates to nucleic acid molecules AAH88708 - AAH88796 isolated from Physcomitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110.
                                                                                                                                                                  Novel moss nucleic acid molecules encoding a carbohydrate metabolis related protein useful for modulating production of fine chemicals as carbohydrates, cofactors and enzymes from microorganisms and pla
                                                                                                                                                                                                                                                                                                   14-DEC-2000; 2000WO-EP12697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         make it a better or more efficient producer of one or more fine chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs having altered activities which indirectly impact the production of one or more desired fine chemicals from plants. Primers AAH88705 - AAH80707 are used in the sequencing of the CMRP cDNA sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                        A gene encoding tick salivary gland antigen - uprotecting animals from tick-carried infections
                                                                     The present sequence represents a tick salivary gland antigen related immunogen. The present invention also describes a tick derived sering protease and a tick derived cysteine protease. A nucleotide sequence encoding any of the above proteins can be used in a vaccine against tick carried infections for domestic animals such as cattle.
                                                                                                                                                                                        WPI; 2000-296340/26.
N-PSDB; AAA29614.
                                                                                                                                                                                                                                                                 17-SEP-1998;
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1.3e+02;
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mammalian
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(LIND/)
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                                                                                                                                                   (FRYK/)
                  protein useful for preparation of vaccines for treatment of
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                                                                 2000-442641/38
DB; AAA30869.
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                                                                                                                                                  JACOBSSON
FRYKBERG L
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LINDMARK H.
                                                                                                                 Lindmark H,
 caused by Streptococcus fibronectin -
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease of the equine upper respiratory tract) caused by S. equinfection. The antibody and/or antiserum may also be used for the prophylactic or the apeutic treatment of S. equi infection in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             especially horses. The use of vaccines containing the fibronectin bindin protein provides a more effective protection against S. equi infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
This invention relates to nucleic acid molecules AAH88708 - AAH88796 isolated from Physcomitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110. Included in the invention is a vector containing the CMRP cDNA, and a host cell transformed with the vector. The host cell (a microorganism, corynebacterium or Brevibacterium, moss or algae or a plant cell) is useful for producing a fine chemical such as carbohydrates, cofactors and/or enzymes. The nucleic acid molecules are suitable for modifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM00097 standard;
                                                                                                                                                                     Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals su as carbohydrates, cofactors and enzymes from microorganisms and plant
                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physcomitrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moss; carbohydrate metabolism fine chemical production; cark
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                                                                                                                                                                                                                                                                                                           (BADI ) BASF PLANT
                                                                                                                              Claim
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| 40 gslggs 45
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                                                                                                                                                                                                                                                                                     Renz A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The use of vaccines containing the fibronectin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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Schmidt R,
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that encodes hemocyanin (II), a domain of (I) or its fragment with the immunological properties of at least one domain of (II). The products (the invention have cytostatic, virucide, antibacterial, antiparasitic, immunomodulatory and antihypertensive activity. (I), and constructs additionally containing antigen-encoding sequences, are useful in gene therapy of tumors. Polypeptides encoded by (I) are useful for treating parasitic or viral infections and tumors, particularly schistosomiasis and carcinoma (of bladder, epithelium, ovary, breast, bronch or colon-rectum), also hypertension, as vaccines, for treating cocaine misuse and very generally as carriers for pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbohydrate production system in a host, e.g., microorganisms and plants. They are also useful to identify those DNA sequences and enzymes in other species which are useful to modify the biosynthesis of starch, cell wall polysaccharides and sugars. The nucleic acid molecules may be utilised in the genetic engineering of Corynebacterium glutamicum and the related Brevibacteium species and Acetobacter xylinum and Chlorella to make it a better or more efficient producer of one or more fine chemicals. Mutagenesis of one or more CNRPs may also result in CNRPs having altered activities which indirectly impact the production of one or more desired fine chemicals from plants. Primers AAH88705 - AAH80707 are used in the sequencing of the CNRP cDNA sequences of the invention.
                                                                                                                                                                                                                                                                                                      WPI; 2000-587517/55
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                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1999;
20-AUG-1999;
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                                       This invention describes a novel nucleic acid molecule (N1) encoding hemocyanin, a hemocyanin domain, or a functional fragment of it with the immunological properties of at least one domain of hemocyanin, and which comprises at least one intron is new. The products of the invention have cytostatic and vasotropic activity and can be used in vaccines or for gene therapy. Compositions comprising nucleic acids of the invention are useful in treating tumors. Compositions comprising hemocyanin polypeptide are useful in treating parasite and viral infections and as an antitumor agent. It is also useful in treating abnormal blood pressure, bladder carcinomas, epithelial carcinomas, ovarian carcinomas, anamany carcinomas, bronchial carcinomas, and colon carcinomas. It may also be used to cure cocating additions.
                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                         Markl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHH1; KLH1; hemocyanin; cytostatic; vasotropic; vaccine; gene therapy; tumor; parasite infection; viral infection; antifumor agent; abnormal blood pressure; bladder carcinoma; epithelial carcinoma; ovarian carcinoma; mammary carcinoma; bronchial carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatics. They may also be used to generate antibodies (Ab). Probes based on (I) and Ab are useful for detecting tumor-specific DNA in a cel (by detecting specific binding to cellular DNA or proteins), particularly where associated with the types of carcinoma listed above. Hemocyanins can be produced recombinantly, relatively inexpensively and in adequate amounts, eliminating the need to culture gastropods. When used as a carrier, (II) significantly increases the half-life of the attached pharmaceutical, by inhibiting ultrafiltration in the kidneys.
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6; Conser
                                                                                                                                                                                                                                                 Page 133-134; 180pp; German.
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                                                                                                                                                               additionally containing antigen encoding sequences, are useful in gene therapy of tumors, polypeptides encoded by (1) are useful for treating parasitic or viral infections and tumors, particularly schistosomiasis and carcinoma (of bladder, epithelium, ovary, breast, bronchi or colon-rectum), also hypertension, as vaccines, for treating cocaine misuse and very generally as carriers for pharmaceuticals, e.g. cytostatics. They may also be used to generate antibodies (Ab). Probes based on (1) and Ab are useful for detecting tumor-specific DNA in a cell (by detecting specific binding to cellular DNA or proteins), particularly where associated with the types of carcinoma listed above. Hemocyanins can be produced recombinantly, relatively inexpensively and in adequate amounts, eliminating the need to culture gastropods. When used as a carrier, (II) significantly increases the half-life of the attached pharmaceutical, by inhibiting ultrafiltration in the kidneys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel nucleic acid (I) containing a sequence that encodes hemocyanin (II), a domain of (I) or its fragment with the immunological properties of at least one domain of (II). The products of the invention have cytostatic, virucide, antibacterial, antiparasitic,
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3.7e+02;
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RESULT AAB71157

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AAB71157

standard; Protein; 416

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                                                                                                                    This invention describes a novel nucleic acid molecule (NI) encoding hemocyanin, a hemocyanin domain, or a functional fragment of it with the immunological properties of at least one domain of hemocyanin, and which comprises at least one intron is new. The products of the invention have cytostatic and vasotropic activity and can be used in vaccines or for gene therapy. Compositions comprising nucleic acids of the invention are useful in treating tumors. Compositions comprising hemocyanin polypeptide are useful in treating parasite and viral infections and as an antitumor agent. It is also useful in treating abnormal blood pressure, bladder carcinomas, petithelial carcinomas, ovarian carcinomas, mammary carcinomas, bronchial carcinomas, and colon carcinomas. It may also be used to cure cocaine addiction.
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                         Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                        Markl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOS-) BIOSYN ARZNEIMITTEL GMBH
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|gslggs 403
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                           Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        Altenhein B,
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                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
              Zea mays subsp. mays
                                              termination sequence;
                                                                                                                                     18-OCT-2000 (first entry)
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                                                                                                           protein
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ilarity 100.0%;
Conservative (
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Pred. No. 3.7e+02;
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                                                                               protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.
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99US-0161920
99US-0161993
99US-0161993
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99US-0159329
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                                                                                                                                                                                                                                                                                   pleuropneumoniae strain
                                                         95ES-0000592.
                                                                                               96EP-0870033
                                                                                                                                                                                                           //label= Sig_peptide
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             protein 1; Tbp1; vaccine; antibody; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB Pred. No. 4.3); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 4.3e+02; thes 0;
                                                                                                                                                                                                                                                                                         1371 serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
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RESULT 1
AAW31346
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Best Local Similarity
****hes 6; Conserve
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  PRESENTATION OF THE PRESEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferrin binding protein 1 (Tbp1) (AAW04867) of Actinobacillus pleuropneumoniae (App) strain 1370, derived from strain Hpn·1 (ATCC 27088) of serotype 1, is probably a transmembrane protein that serves as a channel for transport of iron across the outer membrane. Its amino acid sequence was deduced from a gene (AAT38071) obtd. from App genomic DNA. Recombinant Tbp1, or its antigenic fragments, can be produced in transformed host cells. It is used to formulate vaccines against porcine pleuropneumonia, to prepare antibodies (useful for serotherapy) and to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae transferrin binding protein 1 - production of antibodies useful diagnostically and in universal vaccine against porcine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-427056/43.
N-PSDB; AAT38071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 10-17; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daban M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31346 standard; Protein; 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSecKS; tumour suppressor gene; rat; protein kinase C; mitosis; cancer; malignancy; cell proliferation; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW31346;
                                                                                                                                                                                                                                                                                           Misc-difference
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                     Region
                                                                  Peptide
                                                                                                           Peptide
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                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                             /note=
785
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                                                                                                                                                                                                                                                                                                                                      /note- "encoded by GTC" 757
                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "encoded by TCT" 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                  /note- "1
289..292
                                                                                                               /note= "0
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                                                                                                                                                                                                                                                                                                              "encoded by CCC"
                                                                                                                                                                                                                                                                        encoded by
                                                                                                                                                                                "nuclear localisation
                                                                                                                                                                                                                             "glycine-rich region"
                                               "nuclear
                                                                                            "nuclear
                                                                                                                                  "glycine-rich region"
"glycine-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 17; I
Pred. No. 8.6e+02;
Pred. No. 8.6e+02;
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                                               localisation
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                                                                                            localisation
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                                               signal"
                                                                                          signal"
                                                                                                                                                                                  signal*
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                                                                                                  RESULT 14
AAW31347
                                                                                                                                                                                                                           This polypeptide comprises an active truncated form of the novel tumour suppressor protein SSecKs that is a substrate of protein Standard Can Anhibitor of the transformed phenotype. Its amino acid sequence was deduced from a partial cDNA clone (see AAVO2301) obtained from SC NIH373 cells. The full-length SSeCKS sequence (see AAWO2301) is also provided. Full-length SSeCKS uncleic acid (see AAVO2301) as well as composited proteins encoded by such nucleic acids are claimed, as are isolated proteins encoded by such nucleic acids, vectors comprising the nucleic acids, host cells, and methods of inhibiting the expression of a transformed phenotype in a host cell by introducing the nucleic acids. Introduction of a SSecKS nucleic acid or gene allowing the treatment of diseases associated with disorders of cytoskeletal structure and cellular architecture (such as Alzheimer's disease), and may be a marker for aberrancies in
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                   Matches
        SSECKS: tumour suppressor gene; rat; protein kinase C; mitosis; cancer; malignancy; cell proliferation; Alzheimer's disease;
     therapy
                                    Rat tumour suppressor protein SSeCKS
                                                      20-JUL-1998
                                                                        AAW31347;
                                                                                     AAW31347 standard; Protein; 1596
                                                                                                                                                                                                            Sequence
                                                                                                                                  960
                                                                                                                                                                                                                                                                                                                                                                                             Example 6; F1g 3A-G; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene SSeCKS - used as a mitotic regulator, and inhibitor of malignant phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelman I, Jaken S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1996;
19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GELM/) GELMAN I.
(JAKE/) JAKEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1997.
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                                                                                                                                          1 GSLGGS 6
                                                                                                                                 gslggs
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                                                                                                                                                                  Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV02301.
                                                                                                                                                                                                                          and/or nervous
                                                                                                                                                                                                           1346
                                                                                                                                  965
                                                                                                                                                                  Conservative
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0665401.
96US-0635121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US06830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368.371
/note= "nuclear localisation signal"
1013.1035
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                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "zinc finger"
                                                                                                                                                                                                                        system development.
                                                                                                                                                                 0
                                                                                                                                                              Score 30; DB 18;
Pred. No. 1.3e+03;
; Mismatches 0;
                                                                                      ₹
                                                                                                                                                                              Length 1346;
                                                                                                                                                               Indels
                                                                                                                                                             0,
                                                                                                                                                             Gaps
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This polypeptide comprises the novel tumour suppressor protein SecKs that is a substrate of protein kinase C and which acts as a conspative regulatory of mitosis and as an inhibitor of the transformed phenotype. Its amino acid sequence was deduced from an C isolated nucleic acid molecule (see AAV02302). The SecKs nucleic acid, as well as homologous and hybridising nucleic acids are claimed, as are isolated proteins encoded by such nucleic acids, cettors comprising the nucleic acids, host cells, and methods of inhibiting the expression of a transformed phenotype in a host cell by introducing the nucleic acids. Introduction of a SecKs nucleic acid or gene product into a host cell inhibits mitosis of the host cell, allowing the treatment of diseases associated with disorders of proliferation and/or with the expression of a malignant of cytoskeletal structure and cellular architecture (such as also be used to treat or identify disorders account of a self-complete control of a self-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 11A-L; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene SSeCKS - used inhibitor of malignant phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gelman I, Jaken S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV02302
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(JAKE/) JAKEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1996;
19-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0665401
96US-0635121
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1399..1421
'mote= "zinc finger"
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517..520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "proposed site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "proposed protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "glycine-rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "proposed site"
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system development
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RESULT :
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                   Novel HTLV1 and HTLV2 peptides are disclosed for use in diagn assays for detecting HTLV1 and HTLV2 infection in human sera. Peptides of the invention are given in AARS7055-56.
                                                                                                                                                                                                                                                                                                                                                                                         HTLV-I and -II peptide(s) and kits contg. them - used to diagnose infection and discriminate between HTLV-I and -II infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR57055 standard;
                        gene
                                  Human; 5' EST;
                                                         Human
                                                                                 06-OCT-2000
                                                                                                                              AAG01209 standard; Protein; 97
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 74; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-279743/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fong SKH, Goh C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9418322-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTLV1; HTLV2; HTLV-I; HTLV-II; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTLV peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR57055;
                                                                                                         AAG01209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC.
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                                                                                                                                                                                       10 gsmggs 15
                                                                                                                                                     16
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                                                                                                                                                                                                   1 GSLGGS 6
                      therapy;
                                                         secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.
                                                                                                                                                                                                                                                                                               21 AA;
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                                                                                                                                                                                                                                     Conservative
                                                                               (first entry)
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                    ; expressed sequence tag; secreted protein; \operatorname{cDNA} isolation; \operatorname{chromosome} mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9308-0014153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US01170
                                                         protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hadlock KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                93.3%;
83.3%;
                                                         SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
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Pred. No.
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Pred. No. 1.5e+03;
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                                                          5290.
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39;
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                                                                                                                                                                                                                                                          Length 21;
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                                                                                                                                                                                                                                                                                                                                 diagnostic sera. 2
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Best Local Similarity
Thehes 5; Conserve
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                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                        AAG74477
                                                                                                                                                                                                                                                                                 RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a polypeptide encoded by one of a large number of 5'. ESTs derived from mRNAs encoding secreted proteins. The 5'. ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5'. TR is rarely included. 5'. ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5'. ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
N-PSDB; AAC01215.
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                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                           AAG74477 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; SEQ ID 5290; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards
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                      29-SEP-1999;
03-NOV-1999;
                                                                               05-APR-2001
                                                                                                                              Homo
                                                                                                                                                                                                                                     AAG74477;
                                                        28-SEP-2000;
                                                                                                     WO200122920-A2
                                                                                                                                                    colorectal carcinoma
                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                    Human colon cancer antigen protein SEQ ID NO:5241
(HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                   34 gsiggs
                                                                                                                                                                                                                                                                                                                                           1 GSLGGS 6
                                                                                                                             sapiens.
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                                                                                                                                                                                                             (first entry)
                                                         2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                      99US-0157137
99US-0163280
                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                               93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 21;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, therapy and treatment of diseases associated with inappropriate P cytostatic of the prevention.
N-PSDB;
            WPI; 1998-506734/43
                                          Muller-Cohn J, Narva
                                                                      (MYCO )
                                                                                                  13-MAR-1997;
                                                                                                                                13-MAR-1998;
                                                                                                                                                                17-SEP-1998
                                                                                                                                                                                             WO9840490-A1
                                                                                                                                                                                                                          Bacillus thuringlensis
                                                                                                                                                                                                                                                        Helicoverpa
                                                                                                                                                                                                                                                                                  HD525 toxin; PCR; primer;
                                                                                                                                                                                                                                                                                                                Amino acid sequence of lepidoteran-active HD525 toxin
                                                                                                                                                                                                                                                                                                                                                02-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                      AAW75774 standard; Protein; 633 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 6914-6915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding
                                                                                                                                                                                                                                                                       lepidoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 gsiggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSLGGS
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                                                                      MYCOGEN
AAV52611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 AA;
                                                                                                                                                                                                                                                      ; PCR; primer; amplification; Bacillus
; pest; pesticide; Ostrinia nubilalis;
zea; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                  97US-0040512
                                                                                                                                  98WO-US05081
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                                        ΚE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9803pp;
                                        Schnepf HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 22;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Œ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 119
                                                                                                                                                                                                                                                                   thuringiensis; probe; Heliothis virescens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT
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Best Loc
Matches
            polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation
                                                    This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The new t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                              Claim
                                                                                                                                                        controlling lepidopteran pests, espe
Heliothis virescens and Helicoverpa
                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                             Muller-Cohn J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               lepidoptera; pest; pesticide; (Helicoverpa zea; hybridisation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8612 toxin; PCR; primer; amplification; Bacillus thuringiensis; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis viro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW75775 standard; Protein; 633
                                                                                                                                                                                      New insecticidal Bacillus thuringiensis toxins - useful
                                                                                                                                                                                                                                                                                         (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                      13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                   13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW75775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of lepidoteran-active 8612 toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Pages 32-34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 gsiggs
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DB; AAV52612.
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                                                                                                                           5; Pages 36-38; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxins are useful as pesticides, especially for the control of a nubilalis, Heliothis virescens, and Helicoverpa zea. The lectide coding accommon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 83.: 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequence of a novel Bacillus thuringiensis toxin method of the invention, to control lepidopteran nests
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                                                                                                                                                                                                                                                                                                                      97US-0040512
                                                                                                                                                                                                                                                                                                                                                   98WO-US05081.
                                                                                                                                                                                                                                                             Narva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%;
                                                                                                                                                                                                                                                             KΕ,
                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 19;
Pred. No. 1.4e+03;
1; Mismatches 0
                                                                                                                                                                       especially Ostrinia nubilalis,
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                                                                                                                                                           zea
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Similarity 83.3%;
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h 93.3%;
Similarity 83.3%;
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RESULT

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          (first entry)
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99US-0158029
99US-0158369
99US-0158369
99US-0159294
99US-0159294
99US-0159329
99US-0159331
99US-0159331
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99US-0159637
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99US-0152363.

99US-0153758.

99US-0154018.

99US-0154018.

99US-0154019.

99US-0154779.

99US-0155486.

99US-0155459.
                                                                                                                                                             99US-0160981

99US-01610989

99US-0161404

99US-0161405

99US-0161356

99US-0161356

99US-0161361

99US-0161361

99US-0161361

99US-0161920

99US-0161992
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99US-0160815.
99US-0160980.
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99US-0156596.
99US-0157117.
99US-0157753.
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                                           Protein;
                                                                                                                             93.3%;
                                           67
                                                                                                                   Score 28; DB
Pred. No. 4.5e
1; Mismatches
                                           3
                                                                                                                            DB 21;
4.5e+03;
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                                                                                                                                   Length 1944;
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                                                                                                                                                                                             RESULT
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                             AAG27140 standard; Protein;
                                                                                                                                                                                                                                                                                               Sequence
                         25-FEB-2000; 2000EP-0301439
                                          06-SEP-2000
                                                         EP1033405-A2
                                                                                                                           Zea mays protein fragment SEQ ID NO: 31861.
                                                                                                                                           17-OCT-2000
                                                                                                                                                             AAG27140;
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                                                                         mays subsp.
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(first entry)

91

8

99US-0121825 99US-0123180

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Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                                  Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                                     Guigueno A;
                                                                                                                                                                                                                                                                                Gicquel B,
                                                                                                                                                                                                                                                                                                                              11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
                                                                                                                                                                                                                                    N-PSDB; AAX34007
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
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                                                                                                                                                                                                                                               1999-181045/15.
                                                                                                                                                                32;
 Similarity 83. 5; Conservative
                                                                                                                                                             Fig 2;
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97FR-0010404
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            90.0%;
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Score 27; DB
Pred. No. 2e+0
1; Mismatches
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          DB 20;
2e+02;
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9908-0125788 9908-0126268 9908-0126268 9908-0126268 9908-0128234 9908-0130449 9908-0130449 9908-0132486 9908-0132486 9908-0132486 9908-0132487 9908-0134218 9908-0134218 9908-0134286 9908-0134286 9908-0134286 9908-0134286 9908-0134286 9908-0134286 9908-013428 9908-013428 9908-013428 9908-013428 9908-013428 9908-013428 9908-0136021 9908-0139451 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0139453 9908-0140823 9908-0140823 9908-0140823 9908-0140823 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863 9908-0142863
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Best Local
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21-OCT-1999;
21-OCT-1999;
                                                                                                                               antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; infection; skin aging; cocular disorder; wound healing; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-1999;
07-OCT-1999;
08-OCT-1999;
12-OCT-1999;
        (HUMA-) HUMAN GENOME SCI INC
                           09-APR-1999;
14-JAN-2000;
                                                       06-APR-2000; 2000WO-US09070
                                                                           19-OCT-2000
                                                                                                                                                                                        Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                 Human
                                                                                              WO200061628-A1
                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                         AAB45378 standard;
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26-OCT-1999;
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25-OCT-1999;
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21-OCT-1999;
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18-OCT-1999;
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13-OCT-1999;
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gslgga
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5; Conserv
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                          99US-0128695.
2000US-0176052.
                                                                                                                                                                                                                                  (first entry)
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990S-0160989
990S-0161404
990S-0161405
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990S-0161360
990S-0161361
990S-0161361
990S-0161992
990S-0161992
990S-0161992
990S-0161993
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990S-0160980.
990S-0160981.
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990S-0159584
990S-0160741
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990S-0160814
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99US-0159295.
99US-0159329.
99US-0159330.
99US-0159331.
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99US-0158029.
99US-0158232.
                                                                                                                                                                                                              protein sequence encoded by gene 38 SEQ
                                                                                                                                                                                                                                                                          Protein; 121
                                                                                                                                                                                                                                                                                                                                                                          90.0%;
                                                                                                                                                                                                                                                                                                                                                               Score 27; DB Pred. No. 2.8e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 91
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                                                                                                                                                                                                               ID NO:130.
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Sequence

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cc invention. Human secreted proteins have activities based on the tissues can decils the genes are expressed in. Examples of activities include: and cells the genes are expressive; antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; notropic; comeuroprotective; antibacterial; virucide; fungicide; ophthalmological; comeuroprotective; antibacterial; virucide; fungicide; ophthalmological; cand vulnerary. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a condition of susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a condition of the susceptibility of and coular disorders. The polypeptides can also be used to aid wound healing and coular disorders. The polypeptides can also be used to supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The content of components. AAC80107 to AAC801085 and AAB45307 represent sequences used in the assemblification of the assemblification of the assemblification.
The polynucleotide sequences given in AAC81086 to AAC81134 encode the human secreted proteins given in AAB45308 to AAB45355. AAB45357 to AAB45384 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues
                                                      components. AAC8107 the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or amellorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454pp; English.
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                                                   the present invention.
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Matches 5
                                                                           17-APR-1998;
                                                                                                                                                                                                                                                                                              DE19817948-A1
                                                                                                                                               17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             Endometrium; human;
treatment; uterine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human endometrium tumour EST encoded protein 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59979 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                           98DE-1017948
                                                                                                                                               98DE-1017948
                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour; cancer; anticancer; cytostatic;
gene therapy; expressed sequence tag.
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No.
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3.8e+02;
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(META-) METAGEN GES GENOMFORSCHUNG MBH.

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RESULT
AAB95004
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C anticancer and cytostatic activity. (A) are used (1) for recombinant

C expression of polypeptides (B) and (il) to isolate complete genes. (B)

CC are used (1) to identify agents suitable for treatment of uterine or

CC endometrial cancer; (il) directly for treating these forms of cancer

CC (including expression from gene therapy vectors) and (iii) for

CC (expressed sequence tags) from a particular tissue type before comparison

CC (expression patterns. This allows a significantly longer fragment of

CC the gene to be revealed, so should reduce the number of fallures

CC associated with the fact that ESTs from different libraries may represent

CC different parts of the same unknown gene, distorting the estimated

CC frequency of occurrence in a particular tissue. Axy59941-Y60328 represent

CC correct fragments encoded by the human endometrium tumour cDNA library

CC derived EST fragments represented in AxZ41981-Z42121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                        29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences expressed in uterine cancer tissues, derived polypeptides, for treatment of uterine and endometrial and identification of therapeutic agents
                                    Ota T, I
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB95004 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                  (HELI-) HELIX RES INST.
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                                    Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
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                                                                                                                                        99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                    2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                          99JP-0248036
                                      Nishikawa T,
T, Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO:16665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27;
Pred. No.
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                                    Hayashi K, :
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Β,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid (cDNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4e+02;
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                                        Salto K,
(, Otsuki
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                                                           Yamamoto
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CC sequence and an oligonucleotide which comprises a 5'-end CC polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC CNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification CC of the present invention.
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 16665;
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AAW53009
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Best Local S
Matches S
                       Chen CMA,
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                                                                                                                       Mus musculus
                                                                                                                                       I-mfc; inhibitor of MyoD family; treatment; diagnosis; myogenesi
defects; abnormal development; disease; cleidocranial dysplasia;
CDD; rhabdomyosarcoma; muscle tissue cancer.
                                                                                                                                                                       Mus musculus
                                                                                                                                                                                        03-AUG-1998
                                                                                                                                                                                                        AAW53009
                                                                                                                                                                                                                        AAW53009 standard; Protein; 163 AA
       WPI; 1998-179377/16
                                      (HUTC-) HUTCHINSON CANCER RES
                                                       27-AUG-1996;
                                                                       21-AUG-1997;
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5; Conserv
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                                                                                                                                                                       I-mfc protein.
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                        Z,
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                        Kraut
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Pred. No.
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                                        CENT FRED
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RESULT 29
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence of an I-mf protein or analogue, or for detecting I-mf agonist activity in a test substance. The sequence can be used to treat, model and diagnose defects in myogenesis responsible for abnormal development and disease conditions in mammals, including humans. These include the human disease cleidocranial displasia (CDD), rabdomyosarcomas and other cancers affecting muscle tissue in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pages
AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions,
                                                                                                                                                                                                                                                                                                                                                             04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Respiratory disease; sinusitis; purulent c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1999
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| galggs 125
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                                                                                                                                                                                                                                                      1999-357842/30.
                                                                                                                                                                                 1213; Disclosure; 1912pp; English.
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5; Conserv
                                                                                                                                                                                                                 sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes from the gene sequence can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of MyoD fam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA;
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97FR-0014673
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83
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bronchitis;
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No.
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5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heart disease; sarcoidosis;
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ing I-mf
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RESULT 30
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Best Local S
Matches 5
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
01-APR-1999;
01-APR-1999;
16-APR-1999;
17-APR-1999;
21-APR-1999;
23-APR-1999;
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24-MAY-1999;
11-MAY-1999;
12-MAY-1999;
13-MAY-1999;
13-MAY-1999;
14-MAY-1999;
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11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially where the vector directs the expression of a neutralising epitope of \ensuremath{\mathsf{C}} , pneumoniae.
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46 gtlggs 51
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5; Conserv
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990S-0128234.
990S-0129714.
990S-0129714.
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990S-0130691.
990S-013149.
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990S-01325.
990S-0134218.
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990S-013421.
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990S-0135622.
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990S-0136022.
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83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on; signal transduction pathway; metabolic
genetic mapping; gene expression control;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>--</u>
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5.5e+02;
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promoter;
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02-406-1999;	04-AUG-1999; 04-AUG-1999;	02-AUG-1999; 03-AUG-1999;	02-AUG-1999;	28-JUL-1999; 02-AUG-1999;	27-JUL-1999;	27-JUL-1999;	25-JUL-1999;	23-JUL-1999;	23-JUL-1999;	23-JUL-1999;	22-JUL-1999:	22-JUL-1999;	22-JUL-1999;	21-JUL-1999;	21-JUL-1999;	21-JUL-1999;	20-JUL-1999;	20-301,-1999:	20-301-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	16-JUL-1999:	15-JUL-1999.	14-JUL-1999;	12-JUL-1999;	09-JUL-1999;	08-JUL-1999;	06-JUL-1999;	02-JUL-1999;	01-JUL-1999;	30-JUN-1999;	29-JUN-1999;	28-JUN-1999;	24-JUN-1999:	23-JUN-1999;	22-JUN-1999;	21-JUN-1999;	18-JUN-1999;	18-JUN-1999;	10-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	17-JUN-1999;	16-JUN-1999;	16-JUN-1999;	14-JUN-1999;	10-JUN-1999;	10-JUN-1999;	07-JUN-1999;	04-JUN-1999;	03-JUN-1999:
9905-014/192.	99US-0147204. 99US-0147302.	99US-0146389. 99US-0147038	99US-0146388.	99US-0145951.	99US-0145919.	99US-0145918.	990S-0145276.	99US-0145224.	99US-0145218.	99US-0145145	9905-0145089.	9905-0145087.	9908-0145085.	99US-0145088.	99US-0145086.	99US-0144814.	99US-0144884	9905-0144552.	9905-0144335.	99US-0144334.	99US-0144333.	99US-0144332.	99US-0144331.	99US-0144325.	99US-0144086	99US-0144003.	99175-0144005	99US-0143542.	99US-0142977.	99US-0142920.	99US-0142803.	9905-0142390	99US-0142055.	9908-0141842.	99US-0141287.	99US-0140991.	99US-0140823.	9908-0140354.	99US-0140353.	99US-0139899.	99US-0139817.	9905-0139750.	99US-0139463.	99US-0139462.	99US-0139461.	9905-0139459. 9905-0139460	99US-0139458.	99US-0139457.	9908-0139456.	99US-0139454.	9905-0139492.	9908-0139453.	99US-0139452.	9905-0138847.	990S-0138540.	99US-0138094.	99US-0137724.	990S-0137502.	99115-0137528
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Query Match	28-OCT-1999; 29-OCT-1999;	28-OCT-1999;	26-OCT-1999;	26-OCT-1999;	25-OCT-1999;	25-OCT-1999;	25-OCT-1999;	22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	13-OCT-1999;	13-001-1999;	12-OCT-1999;	08-OCT-1999;	07-OCT-1999;	06-OCT-1999;	05-OCT-1999;	04-OCT-1999;	29-SEP-1999;	28-SEP-1999:	24-SEP-1999;	22-SEP-1999;	20-SEP-1999;	16-SEP-1999;	15-SEP-1999;	13-SEP-1999;	07-SEP-1999;	01-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999;	27-AUG-1999;	26-AUG-1999;	25-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999;	20-AUG-1999:	17-AUG-1999;	16-AUG-1999;	13-AUG-1999;	13-AUG-1999;	11-AUG-1999;	10-AUG-1999;	09-AUG-1999;	09-AUG-1999;	06-AUG-1999;	05-AUG-1999;	
90.0%;	99US-0161993. 99US-0162142.	9908-010	9908-01	9905-01	9908-01	9908-01	9905-01	9905-01	10-8066	99US-01	99US-01	99US-01	99US-01	9905-01	9908-01	99US-01	99US-01	99US-01	99US-01	99US-01	10-5066	TO-SO66	9908-01	9905-01	9905-01	99US-01	9908-01	99US-01	9905-01	99175-01	10-5066	9905-01	9905-01	99US-01	99US-01	9905-01	9908-01	99US-01	9905-01	9908-01	9908-01	9908-01	9905-01	0-2066	99US-01	99US-01	9905-01	9908-01	9905-01	99US-01	9905-01	9908-01	9908-01	99US-01	99US-01	99US-01	0-5066	0-SU66	
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RESULT AAB39461

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AAB39461;

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Best Local Matches

Similarity 5; Conser

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cc vulnerary; anticonvulsant; antibacterial; antirungar; autiparies. CC cardiant. The polynucleotides and polypeptides are useful for preventing, cc cardiant. The polynucleotides and polypeptides are useful for preventing, cc cardiant. The polynucleotides compared to the compared to the polypeptides cc can also be used as a food additive or preservative to increase or cc decrease storage capabilities. The polynucleotide are useful for cc chromosome identification. They are also useful as probes for diagnosing cc adisorder related to the female reproductive system, particularly breast cc and/or ovary cancer. They are also useful in the gene therapy of breast cc and/or ovary cancer. Secreted protein nucleic acids, proteins, cc antibodies, agonists and antagonists are useful in the diagnosis, cc treatment and prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular disorders; (d) wound healing; (e) neurological diseases; cc and (f) infectious diseases such as viral, bacterial, fungal and cc parasitic infections. AAC74328 to AAC74336 and AAB39401 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB39484 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the press invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; immunosuppressive; nootropic; neuroprotective; antiulcer; antiallergic; hepatotropic; antidabetic; antifingal; antiparasitic; artiparasitic; artipar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polynucleotide sequences human secreted proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fifty nucleic acid molecules encoding human secreted proteins, in the prevention, treatment and diagnosis of cancer, immune d cardiovascular disorders and neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 381; 391pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1999; 99US-0126510.
07-JAN-2000; 2000US-0174850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            remale reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    en in AAC/433/ to AAC/4386 encode
AAB39402 to AAB39451, AAB39452 t
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Best Local
                         19-APR 1999
21-APR 1999
23-APR 1999
23-APR 1999
28-APR 1999
30-APR 1999
30-APR 1999
30-APR 1999
06-MAY 1999
06-MAY 1999
06-MAY 1999
11-MAY 1999
11-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-1999;
08-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2000
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95 gslgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000EP-0301439
                      990S-0134370
990S-0134768
990S-0134941
990S-0135124
990S-013523
990S-0135623
990S-0136621
990S-0136392
990S-0136782
990S-0137528
                                                                                                                                                                                                                                                                                                                                                                           990S-0130510
990S-01308911
990S-0131449
990S-0132048
990S-0132487
990S-0132485
990S-0132485
990S-0132485
990S-013425
990S-013421
990S-013421
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990S-013421
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990S-0123548.
990S-0125788.
990S-0126264.
990S-0126785.
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99US-0128234.
99US-0128714.
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99US-0130077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment SEQ ID NO: 14426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
6.1e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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promoter;
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(HUMA-) HUMAN GENOME

05-OCT-2000 WO200058340-A2 Homo sapiens.

WPI;

2000-594638/56.

Ruben SM,

secreted

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04-JUN-1999
08-JUN-1999
08-JUN-1999
10-JUN-1999
11-JUN-1999
11-JUN
990S-0137502.
990S-0138540.
990S-0138540.
990S-0138540.
990S-0139152.
990S-0139453.
990S-0139455.
990S-0139455.
990S-0139457.
990S-0139457.
990S-0139457.
990S-0139460.
990S-0139460.
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990S-0139463.
990S-0140353.
990S-0140353.
990S-0140823.
990S-0140823.
990S-0140823.
990S-0141847.
990S-0144814.
990S-0144337.
990S-0145086.
                                  Query Match
Best Local Similarity
                                06-AUG-1999
06-AUG-1999
09-AUG-1999
10-AUG-1999
11-AUG-1999
12-AUG-1999
12-AUG-1999
12-AUG-1999
12-AUG-1999
13-AUG-1999
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14-AUG-1999
14-AUG-1999
15-SEP-1999
16-SEP-1999
17-AUG-1999
18-CCT-1999
18-CCT-1999
18-CCT-1999
18-CCT-1999
19-CCT-1999
                                99US-0147303
99US-0147403
99US-0147493
99US-0148171
99US-0148341
99US-0148341
99US-0149175
99US-0149426
99US-0149920
99US-0149920
99US-0151066
99US-0151066
99US-0151066
99US-0151303
99US-0151303
99US-0151438
99US-0151438
99US-0151438
99US-0155459
99US-0155469
99US-0155479
99US-0158232
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99US-0159331
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99US-0159637
99US-0159638
99US-0159638
99US-0159638
99US-0160761
99US-0160761
99US-0160815
99US-0160980
99US-0161406
99US-0161360
99US-0161360
99US-0161360
99US-0161360
99US-0161360
99US-0161360
99US-0161360
    83
   Score
Pred.
    27;
    DB 21;
6.2e+02;
              Length
                192;
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us-09-642-660-11.rag
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RESULT :
   RESULT 3
AAW64370
ID AAW6
XX
AC AAW6
XX
OT 09-1
XX
DE Mycc
                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW81735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAW, Twardzik DR, Ved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW81735 standard; Protein; 196
   Mycobacterium tuberculosis antigen XP36.
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic portion of a soluble 
Mycobacterium tuberculosis (MT) antigen which can be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3c; Page 182; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV64530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                       8661-AON-60
                                                                         AAW64370;
                                                                                                       AAW64370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                         190 gsvggs 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                         34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis immunogenic polypeptide XP27 protein #2
                                                                                                                                                                                                                           1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLGGS 6
|:||||
galggs 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
                                                                                                                                                                                                                                                            Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osis; immunogenic; soluble; pharmaceutical; infection;
                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis.
                                                                                                                                                                                                                                                                                                                                                Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0818112
96US-0730510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US18293
                                                                                                         Protein;
                                                                                                                                                                                                                                                                            90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
                                                                                                                                                                                                                                                           Score 27; DB Pred. No. 6.3e 1; Mismatches
                                                                                                                                                                                                                                                              ŗ
                                                                                                         196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vedvick
                                                                                                                                                                                                                                                              6.3e+02;
ches 0;
                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ;
ick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protective immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                           Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                              0
RESULT 35
AAX39167
ID AAX391
XX
AC AAX39
AC AAX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998
                                                                                                                                                                                                                           AAY39167;
                                                                                                                                                                                                                                                              AAY39167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primers.
                       WO9942076-A2
                                                       Mycobacterium tuberculosis
                                                                                     immunotherapy; diagnosis; i
immune response; skin test.
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This polypeptide is encoded by Mycobacterium tuberculosis antigen XR36 DNA (see AAV4421) that was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. XP36 bears no similarity to known sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion a soluble M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Mycobacterium tuberculosis polypeptides and to develop products for the detection of M. tuberculosis and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV44421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                these polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 193-194; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW,
                                                                                                              196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; diagnosis; antigen; xP36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis strain Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0818111
96US-0729622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon
                                                                                                                                                                                                antibodies or oligonucleotide probes and
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DC, Houghton
Twardzik DR,
Score 27; DB 19;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lodes MJ;
                          Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA - used infection
                                                                                                                                                                                                                                                                                                                                                                      of.
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Best Local Similarity 83.3%; Pred. No. 6.3e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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immunisation;

vaccine;

infection;

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RESULT
AAY39024
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                        Antigen; vaccine;
WPI; 1999-527416/44
                                                                     05-MAY-1998;
18-FEB-1998;
                            Campos-Neto A,
                                                                                                      17-FEB-1999;
                                                                                                                           26-AUG-1999
                                                                                                                                                W09942118-A2
                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                   M. tuberculosis recombinant antigen protein XP36 #2.
                                                                                                                                                                                                                                            05-NOV-1999
                                                                                                                                                                                                                                                                                    AAY39024 standard; Protein; 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of
                   Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis. Ag can induce proliferation of, or cytokine secret by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZ19249 to AZ19460 and AAY39083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     part of a Mycobacterium tuberculosis antigen (Ag). Also describe are vaccines and fusion protein containing M. tuberculosis Ag's
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos - Neto
                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                  1 GSLGGS
                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes polypeptides comprising an immunogenic of a Mycobacterium tuberculosis antigen (Ag). Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigens from Mycobacterium tuberculosis useful in diagnostic n tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                       gsvggs 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ĭ,
                                                 CORIXA
                                                                                                                                                                                      diagnosis;
immunity.
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          are used in
                   Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 177-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed
                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۶
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                   tuberculosis
                                                 CORP
                                                                       98US-0072596
98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                     99WO-US03265
                 Dillon DC,
SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0072967
98US-0025197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC,
SG, Skeiky
                                                                                                                                                                                                 detection;
                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                          . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299pp;
                Hendrickson RC, H
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB
Pred. No. 6.3e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hendrickson RC,
YAW, Twardzik
                                                                                                                                                                                               infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR,
                Houghton R;
R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton R; R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                  Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      present
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secretion
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                       Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and disorders such as prostate cancer -
                                                                                 Claim
                                                                                                                                                                                        Rosen
                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                                                                                                                                                                                                                                                                                                       WO200055174-A1
                                                                                                                                                                                                                                                                                                                                               HOMO
                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; rulneray; gastrointestinal; nephrotropic; antiinfective; gynaecologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer antigen protein sequence SEQ ID NO:1529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB56951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB56951 standard; Protein;
                                                                                                                                                                                                               (ROSE/)
                                                                                                                                                                                                                           ( - AMUH )
                                                                                                                                                                                                                                                                                                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   current vaccination strategies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ19119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 223; 323pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 gsvggs 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis infection. The
                                                                                                                                                                 2000-587513/55
                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                       CA,
                                                                                                                                                                                                                                                                                                                                                                     infectious
                                                                                                                                                                                                               ROSEN
                                                                                                                                                      AAF16154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conser
                                                                               Page 1970-1971;
                                                                                                                                                                                       Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                              GENOME SCI INC.
C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and are useful as vaccines for immunizing against is infection. The new detection methods are needed nation strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                  99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                                                    pulmonary;
disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .38;
                                                                            2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                                                                                                                                                        cardioactive; immunomodulatory; muscular; nephrotropic; antiinfective; gynaecological; neural; immune; reproductive; renal; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB
Pred. No. 6.3e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      portions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                               as prostate
diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196;
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proteins, called prostate cancer antigens, given in AAB55363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen

AAF15566 to AAF16505 encode the human prostate cancer associated

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RESULT 38
AAY06887
CC family of polypeptides. Host cells transfected with a vector comprising CC the HWHHJ20 nucleic acid are used for the recombinant expression of the CC polypeptide. The HWHHJ20 nucleic acid may be used as probes or primers to Screen for genetic mutations in, or alterations in the expression of the CC gene, in a patient compared to a healthy individual. This may lead to the CC diagnosis of or identification of a predisposition to diseases such as CC cancer, autoimmune diseases, asthma, rheumatoid arthritis, Alzheimer's CC disease, AIDS and stroke. Similarly measuring the amount of the CC diseases, and stroke. Similarly measuring the amount of the CC diseases. The polypeptide may be used to identify its agonists or antagonists; and to identify membrane-bound or soluble receptors. A CC fusion protein of the HWHHJ20 polypeptide and an IgG heavy chain may be used in therapy, diagnosis and drug screening. The polynucleotide is used cor for gene therapy; for determining genetic linkage, genetic variability or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              888888888x&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                      The invention relates to a HWHHJ20 polypeptide, a member of the pim
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                        and autoimmune
                                                                                                                                                                                                                                                                                                                                                         ¥PI;
                                                                                                                                                                                                                                                                                                                                                                                     Albone EF,
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1997;
24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP911391-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HWHHJ20 polypeptide; pim family; cancer; autoimmune disease; rheumatoid arthritis; Alzheimer's disease; AIDS; stroke; genetic linkage; chromosome localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAF73737 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                        New clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  нwннJ20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06887 standard;
                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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102 galggs 107
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                                                                                                                                                                                                                                                                                                                                                      1999-246411/21.
                                                                                                                                                                                                                                                                                                                                       AAX32973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                           Page 15;
                                                                                                                                                                                                                                                                                        HWHHJ20, use
nune diseases
                                                                                                                                                                                                                                                                                                                                                                                 Kikly KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
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                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0123184.
97US-0063245
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                                                                                                                                                                                                                                                        21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                    useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%;
                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB
Pred. No. 7.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 localisation
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. 7.6e+02;
tches 0;
                                                                                                                                                                                                                                                                                                  and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 233;
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                                                                                                                                                                                                                                                                                                     cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                     AIDS
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RESULT :
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                     The sequence is that of murine I-mfa (inhibitor of MyoD family) protein. Probes from the gene sequence can be used for determining presence of an I-mf protein or analogue, or detecting I-mf agonist activity in a test substance. The sequence can be used to treat, model and diagnose defects in myogenesis responsible for abnormal development and disease conditions in mammals,
                                                                                  including humans. These include the human disease cleidocrania displasia (CDD), rhabdomyosarcomas and other cancers affecting
                                                                                                                                                                                                               Inhibitor of diagnosis of
                                                    Sequence
                                                                         muscle tissue in mammals.
                                                                                                                                                                              Disclosure; Pages 74-75; 92pp; English.
                                                                                                                                                                                                                                                N-PSDB; AAV21282
                                                                                                                                                                                                                                                                                                   (HUTC-) HUTCHINSON CANCER RES
                                                                                                                                                                                                                                                                                                                         27-AUG-1996;
                                                                                                                                                                                                                                                                                                                                              21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                       WO9808860-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                 CDD; rhabdomyosarcoma; muscle tissue cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                             defects;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus I-mfa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW53007
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on chromosomes. The
derived from EST.
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                                                                                                                                                                                                                                                          1998-179377/16
                                                                                                                                                                                                                                                                                CMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor
Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 246
                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal development;
                                                                                                                                                                                                                                                                              Groudine M,
                                                    246
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                                                                                                                                                                                                               MyoD family proteins - defects in myogenesis r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                    AA;
                                                                                                                                                                                                                                                                                                                        96US-0704931.
                                                                                                                                                                                                                                                                                                                                             97WO-US14780
                                                                                                                                                                                                                                                                                                                                                                                                                                         of MyoD family; treatment; diagnosis; l development; disease; cleidocranial (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression; and may also be used to localize genes present sequence represents a HWHHJ20 fragment
         90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%;
                                                                                                                                                                                                                                                                               Kraut N,
         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 20;
Pred. No. 7.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                              Weintraub
         27;
No.

    useful for,
responsible

         DB 19
8e+02;
                   19;
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                                                                                                                                                                                                                e.g. treatment for abnormal
                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
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                   246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r-mfb; inhibitor of MyoD family; treatment; diagnosis; myogenesis;
defects; abnormal development; disease; cleidocranial dysplasia;
CDD; rhabdomyosarcoma; muscle tissue cancer.
                                                                                                                                                                                                                                                                                                                                                               Inhibitor of MyoD family proteins - useful for, e.g. treatment and diagnosis of defects in myogenesis responsible for abnormal development
                                                                                                                                                                                                                                                                                                                                       Disclosure; Pages 77-78; 92pp; English.
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N-PSDB; AAV21283.
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ALIGNMENTS

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01-FEB-1995 (Rel. 31,
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Rapoport G., Danchin A.;
Rapoport G., Danchin G., Schweizer J., Schweizer J
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer
Presecan E., Santana M., Schneider E., Schweizer J., Vertes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SubtiList; BG10562; ywbA.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF02378; PTS_EIIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
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Phosphorylation; Transmembrane; Complete proteome.
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Pfam; PF02378; PTS_EIIC; 1.
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                                                                                                                  TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97124196; PubMed-8969509; Yoshida K., Shindo K., Sano H., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97144536; PubMed-8990303;
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                            or send an
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                                                                                                                                                                                                               Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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                                                                                                                                                                                                                                                                            Z49992; CAA90286.1; -. D83026; BAA11744.1; -. Z99123; CAB15884.1; -.
                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long as its content and this statement is not removed. Usage by an requires a license agreement (See http://www.isb-an email to license@isb-sib.ch).
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
CELLOBIOSE-SPECIFIC IIC COMPONENT
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                                                                                                                                                                                                               system;
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POTENTIAL.
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(See http://www.isb-sib.
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Query Match Best Local S Matches 6

Similarity 6; Conserv

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Score 30; Pred. No. Mismatches

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RESULT 3
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ID HGBC_H
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Q9KIVO;
20-AUG-2001 (Rel. 40, C
20-AUG-2001 (Rel. 40, I
20-AUG-2001 (Rel. 40, I
HEMOGLOBIN BINDING PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.";
Infect. Immun. 68:4092-4101(2000).
-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OF THE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20316037; PubMed-10858226;
Cope L.D., Hrkal Z., Hansen E.J.;
"Detection of phase variation in expression of proteins involved hemoglobin and hemoglobin-haptoglobin binding by nontypeable
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF221060; AAF80178.1; -
                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane;
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  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING. ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A WAY TO AVOID THE INMUNOLOGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY; HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS REQUIRED FOR HEME UPTAKE.
SUBCELLULAR LOCATION: OUTER MEMBRANE
MISCELLANEOUS: THIS PROTEIN IS SUBJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA
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                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG PS01156; TONB_DEPENDENT_REC_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                       Repeat.
                                           Conservative
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                                      Score 30; DE
Pred. No. 1.4
0; Mismatches
                                                                                                                                                    TONB BOX.
TONB C-TERMINAL BOX.
V; A551BF3B2C641612
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3 X 4 AA TANDEM REPEATS OF Q-P-T-N.
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                                                                                                                                                                                                                                                                                                                                                                                    box; Multigene family; Signal;
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RESULT 4
HGP2_HAEIN
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STRAINERD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A. R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerlavage A. R., Bult C.J., Tomb J.-Fields C.A., Gocayne J.D., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
White O., Cla
                                                                                                                                                                                                                                                                                                                                                                                                  Gray C., Fountoulakis M.; "Two-dimensional map of the proteome of Haemophilus influenzae."; Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                         Coudert E.;
Unpublished observations (AUG-2001).
-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN
-!- FUNCTION: ACTS AS OF THE HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE-20137488; PubMed-10675023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White O., Clayton R.A., Kerlavage A.R., Fleischmann Peterson J., Hickey E., Dodson R., Gwinn M.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus inriuente.
Proferia; Profeobacteria;
                                                                                                                                                                                                                                                                                                                                                                                       CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Langen H., Takacs B., Evers S.,
Sray C., Fountoulakis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing influences Rd.":
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE HEMOGLOBIN AND HEMOGLOBIN-HAPTOGLOBI
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EMBL; U32749; AAC22319.1; ALT_SEQ TIGR; H10661; •

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RESULT 5
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087296;

20-AUG-2001 (Rel. 4

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PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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                                                                                                                                                                            "Conservation of hemoglobin/hemoglobin-haptoglobin binding Haemophilus influenzae."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        STRAIN-Ela / Seroty
Morton D.J., Stull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Ren Z., Jin H., Morton D.J., Stull T.L.;
"hgpB, a gene encoding a second Haemophilus influenzae hemoglobin-
hemoglobin-haptoglobin-binding protein.";
Infect. Immun. 66:4733-4741(1998).
                                                                                                                                                                                                                                                                                                                                               STRAIN=H1689 / Serotype B;
MEDLINE=98427137; PubMed=9746572;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HI689
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; P.
Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GSLGGS 195
       SÜBCELLULAR LOCATION: OUTER MEMBRANE.

MISCELLANBOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE

EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAR

REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRI

ADDITION OF LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING

FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF TREPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A

WAY TO ANOID THE IMMUNOLOGICAL RESPONSE OF THE HOST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (APR-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR THE
                                                                                                                                   HEMOGLOBIN/HAPTOGLOBIN COMPLEX OF FOR HEME UPTAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria;
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1 (Rel. 40, Last annotation update)
AND HEMOGLOBIN-HAPTOGLOBIN BINDING
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Stull T.L.;
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PROBABLE HEMOGLOBIN AND HEMOGLOBIN-
HAPTOGLOBIN BINDING PROTEIN 2.
7 X 4 AA TANDEM REPEATS OF Q-P-T-N.
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Pred. No.
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TONB C-TERMINAL BOX.
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PROTEIN FAMILY;
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PROSITE; PSO1156; TONB_DEPENDENT_REC_2; 1.
PROSITE: PSO1156; Transport; TonB box; Multigene family; Signal;
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EMBL; AF259266; AAK51630.1; --
Interpro; IPR000531; TonB_boxc.
Pfam; PF00593; TonB_boxc; 1.
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                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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REPEAT
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SEQUENCE FROM N.A STRAIN-NTHI N182;
                                                          HGBA
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Q9KIV2;
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                                          Bacteria;
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                                                                          20-AUG-2001
20-AUG-2001
                                                                                            20-AUG-2001
                                                                                                                                                                                                                                 SEQUENCE
                        NCBI_TaxID=727;
                                 Haemoph1lus
                                                  Haemophilus
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                                                  influenzae
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8 X 4 AA TANDEM REPEATS OF P-T-N-Q
                                                                                                                                                                                                 Score 30;
Pred. No.
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                                                                                                              PRT;
                                           subdivision; Pasteurellaceae;
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Matches 6
                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA) (LSH-B) (LH-B).
                                                                                                                                                                                                                LSHB_COTJA
P45657;
               Eukaryota; Metazoa; Chordata; C
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                             COTJA
                                    Coturnix coturnix japonica (Japanese quail).
Eukaryota: Metazoa: Chordata: Craniata: Vert
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REPEAT
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hemoglobin and hemoglobin haptoglobin binding l
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hes 6; Conserv
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SUBCELLULAR LOCATION: OUTER MEMBRANE.

MISCELLANBOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING. ADDITION OR LOSS OF CCAA REFEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A WAY TO AVOID THE IMMUNOLOGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY; HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN
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PS01156; TONB_DEPENDENT_REC_2; 1.
PS01156; Transport; TonB box; Multigene family; Signal;
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; Mismatches 0;
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                  Galliformes;
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B C-TERMINAL BOX.
769964335A4ED3C1 CRC64;
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                                      Vertebrata;
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           ebrata; Euteleostomi;
Phasianidae; Phasianinae;
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01-NOV-1997
20-AUG-2001
        Eukaryota; Metazoa; Arumuyouz.
Pterygota; Neoptera; Endopterygota;
Prohydroidea; Drosophilidae; Drosoph
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SIGNAL
                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000359; Cys_knot.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR001545; G1yco_hormone_beta
Pfam; PF00007; Cys_knot; 1.
PRINTS; PR00438; GFCYSKNOT.
SMARP; SM00068; GHB; 1.
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between
                                                                POX-N
                                                                            PAIRED BOX
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HSSP; P01233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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Jen. Comp. Endocrinol.
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[1]
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SUBUNIT: HETERODIMER OF A COMMON ALDHA CHAIN AND A UNIQUE
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
                                                                                                                                                                                        GSMGGS
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POX-NEURO PROTEIN (PAIRED BOX NE
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SPERMATOGENESIS AND OVULATION
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                           Diptera;
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Coll 69:159-172(1992).
[2]
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**POX-neuro is required for development of chemosensory bristles in Drosophila.";

**J. Neurobiol. 32:707-721(1997).

**J. Neurobiol. 32:707-721(1997).

**IP-CRISTION: TRANSCRIPTIONAL REGULATOR THAT SPECIFIES POLY-INNERVATED ORGANS (CHEMOSENSORY BRISTLE). ALSO CONTROLS THE NUMBER OF ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bopp D., Jamet E., Baumgartner s., "Isolation of two tissue-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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EMBL; X58917; CAA41721.1;
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-1- TISSUE SPECIFICITY: CENTRAL AND PERIPHERAL
-1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemosensory organs in Neuron 12:25-34(1994).
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EMBO J. 8:3447-3457(1989).
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                                                                                                                                                                                                                                                                                                                       PROSITE;
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osensory organs in Drosophila.";
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ox; Developmental protein; Nuclear protein; ption regulation; Neurogenesis; Differentiation. 5 130 PAIRED BOX. 146 157 POLY-ALA.
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DR Pfam; PF00587; trNA-synt_pro.

NR PRINTS; PR01046; TRNA-SYNTHPRO.

NR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.

W Aminoacyl-trNA synthetase; Protein biosynthesis; Lig

Complete Proteome.

SEQUENCE 572 AA: 6707E ....
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MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Sprigss T., Hedblom E.C., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
Haemophilus.
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TIGR; H10729; -.
InterPro; IPR002106; AA_tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
- CARLYTIC ACTIVITY: ATP + L-PROLINE - PYRODHOSPHATE + L-PROLINL-TRNA(PRO).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
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SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE) (PRORS).
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P36096;
01-JUN-1994 (Rel. 2
01-JUN-1999 (Rel. 2
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
15-YUL-1997 (Rel. 3)
                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's Eukaryota; Fungl; Ascomycota; Sacc Saccharomycetales; Saccharomycetac; NCBI_TaxID-4932;
       MEDLINE=93127731; PubMed=1481573;
Purnelle B., Skala J., van Dyck L
"The sequence of a 12 kb fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bloinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi S.-K., Shin B.-S., Park S.-H.;
"Nucleotide sequence of a new Bacillus thuringiensis cry2-type gene.";
Submitted (NOY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                     protein
                                                                                                                                                                                                                                         Purnelle
                                                                                                                                                                                                                                                          MEDLINE=94262309;
                                                                                                                                                                                                                                                                                      STRAIN-S288C
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
ERNA gene and four new open reading frames including a leucine zipper
protein and a homologue to the yeast mitochondrial regulator ABF2.";
ceast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; Sporulation. SEQUENCE 633 AA;
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SIMILARITY: BELONGS
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    B., Skala u
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38,
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Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
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    Goffeau A.;
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Best Local
                                                                                                                           STRAIN-972;
Odell C., Churcher C.M., Barrell B.G., Rajandream M.A., Wals Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF CALCIUM (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 - ADP + PHOSPHATE.
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NCBI_TaxID=4896;
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20-AUG-2001 (Rel.
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EMBL; X69584; CAA49298.1; -.
EMBL; Z8034; CAA61869.1; -.
PIR; S37855; S37855
SGD; S0001517; YKL034W.
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the European Bioinformatics Institute.
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                                                                     CATALYTIC ACTIVITY: ATP + H(2)O = SUBCELLULAR LOCATION: INTEGRAL MEM SIMILARITY: BELONGS TO THE CATION (E1-E2 ATPASES). SUBFAMILY IV.
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Matches
                                                                                                                                                                                                                        STRAIN=5288C;

MEDLINE=95282514; PubMed=7762302;

Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;

Vandenbol M. Durand P., Dion C., Portetelle D., Hilger F.;

"Sequence of a 17.1 kb DNA fragment from chromosome X of

"Sequence of a rerevisiae includes the mitochondrial ribosomal
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                                                                                                                                                                                                                                                                                                                                                                         YJG7_YEAST STANDARD: PRT: 116 AA. P40365; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) HYPOTHETICAL 12.7 KDA PROTEIN IN SMC3-MRPL8 I YJL067W OR J1107 OR HRAL16.
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Interpro; IPR001757; E1-E2_ATPa.
Interpro; IPR001454; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
PROSITE; PS00154; ATPASE_E1_E2;
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                                                                        EMBL; 234288; CAA84056.1; -. EMBL; 249342; CAA89357.1; -.
                                                                                                                           entities requires a
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Pred. No. 4.96
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6D5A655ABFA990DF CRC64;
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PHOSPHORYLATION (BY SIMILARITY).

W; E8495A7598B3020B CRC64;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91125140; PubMed=2280689; Drolet M., Zanga P., Lau P.C.K.; Drolet M., Zanga P., Lau P.C.K.; "The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101."; Mol. Microbiol. 4:1381-1391(1990).
                                                                             Bacteria; Proteobacteria;
Azospirillum.
Fani R., Bazzicalupo M., I
Sgaramella V., Polsinelli
                     MEDLINE-89313660; PubMed-2664449
                                    STRAIN-SP6;
                                                                                                     Azospirillum brasilense
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EMBL; X61207; CAA43515.1; --
PIR; JE0045; JE0045.
PIR; S16798; S16798.
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PROSITE; PS00954; IGP_DEHYDRATASE_1;
PROSITE; PS00955; IGP_DEHYDRATASE_2;
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3-PHOSPHATE - 3-(IMIDAZOL-4-YL)-2-OXODROPYL PHOSPHATE + H(2)O.
PATHWAY: SEVENTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE
                               SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                               MCCOUD'S W.K. Jr., Huang T.J., Maines M.D.;
MCCOUD'S W.K. Jr., Huang T.J., Maines M.D.;
MCCOUD'S W.K. Jr., Huang T.J., Maines M.D.;

"Isolation and characterization of a cDNA from the rat brain that encodes hemoprotein heme oxygenase-3.";

Eur. J. Biochem. 247:725-732(197).

-1- FUNCTION: HEME OXYGENASE CLEAVES THE HEME RING AT THE ALPHA METHENE BRIDGE TO FORM BILIVERDIN. BILIVERDIN IS SUBSEQUENTLY METHENE BRIDGE TO FORM BILIVERDIN BEDUCTASE. HEME OXYGENASE CONVERTED TO BILIRUBIN BY BILIVERDIN REDUCTASE. HEME OXYGENASE CONVERTED TO BILIRUBIN BY BILIVERDIN REDUCTASE.
                                                                                                                                                                                             This SWI
between
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15-DEC-1998
30-MAY-2000
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O70453;
                                                                       Pfam; PF01126; Heme_oxygenase;
                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  the
                                                                                                    EMBL; AF058787; AAC14142.1;
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Streptomycin biosynthesis
SEQUENCE 281 AA; 31726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                               ween the Swiss Institute of Bioinformatics and the I
European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE HEME OXYGEN/
SIMILARITY: CONTAINS 2 HEME REGULATORY
                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: FOUND IN THE
HEART, KIDNEY, BRAIN AND TESTIS.
                                                                                                                                                                                                                                                                                          CO + 3 A + 3 H(2)O.
SUBCELLULAR LOCATION: MICROSOMAL.
                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: HEME + 3
Oxidoreductase; Microsome; Multigene
N 238 243
N 255 260 HRM 2 (200 NCE 290 AA; 3260
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                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
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5; Conser
                                                                                   IPR002051; Heme_oxygenase.
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(Rel. 37, Last sequence upd
(Rel. 39, Last annotation u
(ASE 3 (EC 1.14.99.3) (HO-3).
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Rodentia;
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      HRM 1 (PROBABLE).
HRM 2 (POTENTIAL).
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Pred.
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, Maines M.D.;
~DNA from t
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Matches 5
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                                                                                                                               PRINTS; PROMO39; HTHLYSR. FAMILY; 1. PROSITE; PS00044; HTHLYSR. FAMILY; 1. PROSITE; PS00044; HTHLYSR. FAMILY; 1.
                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Belcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               050683;
30-mAY 2000 (Rel. 39, Created)
30-mAY 2000 (Rel. 39, Last sequence update)
30-mAY 2000 (Rel. 40, Last annotation update)
40, Last annotation update)
410, Last annotation Resultantor RY2282C.
410, RY2282C OR MT2340 OR MTCY339.28.
411, Mycobacterium tuberculosis.
412, Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                     EMBL; 277163; CAB00986.1; -. EMBL; AE007077; AAK46624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to -1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987;
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NCBI_TaxID-1773;
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nterPro; IPR000847; HTH_LysR
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Similarity 83.3%;
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1; Mismatches
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99013870; Puk
Gibbs L., Willis D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                     DOMAIN
                                                                                                                                                                Pfam; PF01126; Heme_oxygenase; PRINTS; PR00088; HAEMOXYGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *The identification and expression
                                                                                                                   ieme;
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 GSLGGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUESTRATED AND DESTROYED.

FUNCTION: HEME OXYCENASE 2 COULD BE IMPLICATED IN THE FUNCTION: HEME OXYCENASE 2 COULD BE IMPLICATED IN THE OF CARBON MONOXIDE IN BRAIN WHERE IT COULD ACT AS A NEUROTRANSMITTER.

CATALYTIC ACTIVITY: HEME + 3 AH(2) + O(2) - BILIVERDICO + 3 A + 3 H(2)O.

SUBCELLULAR LOCATION: MICROSOMAL.

SIMILARITY: BELONGS TO THE HEME OXYGENASE FAMILY.

SIMILARITY: CONTAINS 2 HEME REGULATORY MOTIFS (HRM).
                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is formatically the content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSLGGS
                                                                                             TE; PS00593; HEME_OXYGENASE; 1.
Oxidoreductase; Microsome; Multigene
NG 44 44 PROXIMAL HEME
                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                              IPR002051; Heme_oxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of mouse heme oxygenase-2."; (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
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       35738
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       ¥.
Some: Multigene family.
PROXIMAL HEME LIGAND (
HRM 1 (POTENTIAL).
HRM 2 (POTENTIAL).
RAL -> SSS (IN REF. 2)
RAL -> SSS (IN CREF. 2)
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CRC64;
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Cruse I., Maines M.D.;
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Evidence suggesting that the two forms of the suggesting products of different genes, "

1. Biol. Chem. 263:3348-3353(1988).

1. FUNCTION: Chem. 263:3348-3353(1988).

1. FUNCTION: CHEME OXYGENASE IS SUPPRIOR OF THE ACTIVITY OF HEME OXYGENASE IS OWNER OF THE ACTIVITY OF HEME OXYGENASE IS OWNER OF THE ACTIVITY OF THE ACTIVITY
            EMBL; J05405; AAA41340.1; -. EMBL; U05013; AAA19130.1; -. EMBL; U05018; AAA41347.1; -.
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88139412; PubMed=3343248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 142-232 FROM N.A.,
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P23711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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J. Biol. Chem. 265:7501-7506(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rotenberg M.O., Maines M.
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INDUCTION: HEME OXYGENASE 2 ACTIVITY IS NON-INDUCIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: HEME + 3 AH(2) + CO + 3 A + 3 H(2)O. SUBCELLULAR LOCATION: MICROSOMAL.
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1. 20, Last sequence update)
1. 39, Last annotation update
2 (EC 1.14.99.3) (HO-2).
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MEDLINE-95292107; PubMed-7773790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces scabies.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRSC
                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scabies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cioning, sequencing, and regulation of expextracellular esterase gene from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91072254; PubMed=2254271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTERASE PRECURSOR
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PIR; A35199; A35199.
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274 GTLGGS 279
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                                                                                                                                                   A37845; A37845
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Oxidoreductase; Microsome; Multigene
Oxidoreductase; Mrcrosome; Multigene
                                                                                                                      LESC;
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15-OCT-95.
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Serine esterase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
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(Rel. 19, Last sequence update)
(Rel. 35, Last annotation update)
ECURSOR (EC 3.1.1.-).
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                         Signal; 3D-structure
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HRM 2 (POTENTIAL).
QNEPE -> EFRNK (IN |
MQI -> TEF (IN REF.
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Pred. No. 1.8e+02;
1; Mismatches (
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QI -> TEF (IN REF. 3).
981AADE01DE1AFCF CRC64;
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Golil S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolæva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Seller McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.T., Ventrona Straser C.M.;
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15-JUL-1998 (Rel. 3
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
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032445; Q9K
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20-AUG-2001 (Rel. 40, Last annotation update)
N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (
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NAGA OR VC0994.
                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                  Hydrolase;
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PATHWAY: N-ACETYL GLUCOSAMINE UTILIZATION
SIMILARITY: BELONGS TO THE NAGA FAMILY.
                                                                                                                                                                                                                                                                                                                                      ure 406:477-483(2000). CATALYTIC ACTIVITY: N
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AE004181;
VC0994; -.
                                                Pro; IPR003764; NagA.
PF02612; NagA; 1.
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N., Oura N., Wang J., Fujishima S.;
ng and sequencing of the genes for N-acetylglucosamine use
uct divergent operons (nagE-nagAC) from Vibrio cholerae
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01-JUN-1994
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Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnollophyta; eudicotyledons;
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PROSITE; PS00502; POLYGALACTURONASE;
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MEDLINE-94289651; PubMed-8018876;
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Matches 5
                                                                             Malherbe P., Richards J., Gaillard H., Thompson A., Diener (Schuler A., Huber G.;

"CDNA cloning of a novel secreted isoform of the human Reception and Glycation End products (RAGE) and characterization co-expressing cell-surface scavenger receptors and Swedish manyloid precursor protein.":
                                                                                                                                                                                                                                                                                                                                                                                           Banta A.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neeper M., Schmidt A.M., Brett J., Yan S.D. Elliston K., Stern D., Shaw A.; "Cloning and expression of a cell surface glycosylation end products of proteins."; J. Biol. Chem. 267:14998-15004(1992).
                                                                                                                                                                                                                                               endproducts.";
Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the class II: gene for receptor of advanced products, PBX2 homeobox gene and a notch hon of mouse mammary tumor gene into
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SEQUENCE OF 1-12 FROM N.A. Hudson B.I., Futers T.S.;
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Submitted (MAY-1999) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-95137587; PubMed-7835890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92340547; PubMed-1378843; Meaper M., Schmidt A.M., Brett J.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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5; Conservative
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23:408-419(1994).
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B3A486FB281E492B CRC64;
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 2.
SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_like; 1.
PR0SITE; PS00290; IG_MHC; 1.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Glycoprotein; Transmembrane;
Alternative splicing; Polymorphism.
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TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J; M91211; AAA03574.1; -..., D28769; BAA05958.1; -..., U89336; AAB47491.1; -..., AB036432; BAA89369.1; -..., AJ133822; CAB43108.1; -..., AF208289; AAG35728.1; -...
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
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Ig_c2.
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
Score 27; DB Pred. No. 2.3e 1; Mismatches
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                      DB 1;
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        YCDG_ECOLI STANDARD;
P75892; O9R3W5;
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20-AUG-2001 (Rel. 40, Last
PUTATIVE PURINE PERMEASE Y
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Pfam; PF00083; sugar_tr; 1.
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or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                  Hypothetical
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P55705;
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T PROTEIN Y4XM.
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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A 7.18-kb DNA sequence of the Escherichia coli K-12 genome ra 7.18-kb DNA sequence of the 20.7-28.0 min region on the linkage map. CONA Res. 3:137-155(1996).

INTEGRAL MEMBRANE PROTEIN (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000202; AAC74091.1; ALT_INIT. EMBL; D90737; BAA35773.1; -. EMBL; D90738; BAA35783.1; -.
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                                                                                                                                                                                                                                                                                                                                      Hypothetical TRANSMEM
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PROSITE; PS01116; XANTH_URACIL_PERMASE;
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    -1- SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.

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                                                                 297
                                                                                        1 GSLGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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on the linkage map.";
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STANDARD;

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J. Lipid Res. 36:1305-1314(1995).

J. Lipid Res. 36:1305-1314(1995).

-i- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARPERIAL MALLS DURING ATHEROCENESIS. TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).

-i- SUBUNIT: HOMOTRIMER.
-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND II; ARE PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                                             Aftring R.P., Freeman M.W.;
Structure of the murine macrophage so evaluation of sequences that regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Freeman M., Ashkenas J., Rees D.J., Kingsley D.M., Copeland N.G., Jenkins N.A., Krieger M.;
Jenkins N.A., Krieger M.;
An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 349-458 FROM N.A. MEDLINE-91062370; PubMed-1978939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rateri D.L., Whitman S.C., Block A.E., Daugherty A.; "Identification of a functional domain in class A scave that mediates metabolism of AcLDL."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Charged collagen structure mediates the recognition of necharged macromolecules by macrophage scavenger receptors."

J. Biol. Chem. 268:2126-2133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93131972; PubMed-8380569;
Doi T., Wada Y., Kodama T., Higashi K.I.,
Miyazaki T., Nakamura H., Uesugi S., Imani
Itakura H., Yazaki Y., Matsumoto A.;
                                                                                                                                                                                                                                                                                                                                                                                    cell line, P388D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structures and high and low affinity ligand binding properties murine type I and type II macrophage scavenger receptors."; J. Lipid Res. 34:983-1000(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30204; Q9QZ56;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED LDL RECEPTOR I AND II) (SCAVENGER RECEPTOR TYPE A) (SR-A).
MSR1 OR SCVR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95395388; PubMed-7666008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors."
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SEQUENCE FROM N.A. (ISOFORMS I AND MEDLINE-93359822; PubMed-8394868;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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   L04274;
L04275;
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                  AAA39747
ALT_INIT.
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te expression in the macrophage
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Imanishi T., I
                                                            (See http://www.isb-sib.ch/announce,
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RESULT 28
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Lieman-Hurwitz J., Ronen-Tarazi M., Gabai C., Hassidim M.,
Schwarz R., Kaplan A.;
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE LIGHT-INDEPENDENT REDUCTION PROTOCHLOROPHYLLIDE (PCHLIDE) TO CHLOROPHYLLIDE (CHLID
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                                                                                                                                                                                              CHLN.
                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE SUBUNIT
CHE 1.3.1.33) (LI-POR SUBUNIT N) (DPOR SUBUNIT N).
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NCBI_TaxID=1140;
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PROSITE; PS50287; SRCR_2; 1.
Transmembrane; Glycoprotein;
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SMART; SM00202; SR;
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ACTIVITY: CHLOROPHYLLIDE A +
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cteria: Chroococcales; Synechococcus.
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MISSING (IN ISOFORM II).
V -> L (IN REF. 3).
N -> K (IN REF. 3).
A -> E (IN REF. 3).
A -> E (IN REF. 3).
C -> E (IN REF. 3).
U -> N (IN REF. 3).
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Photosynthesis; Chlorophyll biosynthesis; Oxidoreductase;
Photosynthesis; S1540 MW; 9BIA51305045574C CRC64;
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                                                                                                                                                                                                                                                                                                                                           Wang X., "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                Ando S., Tokui T., Yano T., Inaggki M.;
Biochem Blophys, Res. Commun. 221:67-71(1996).

-!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
-!- KERATIN B ASSOCIATES WITH KERATIN 18.
-!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)

(40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92129304; PubMed-1370816;
Hsieh J.-T., Zhau H.E., Wang X.-H., Liew C.-C., Chung L.W.K.;
Regulation of basal and luminal cell-specific cytokeratin express.
In rat accessory sex organs. Evidence for a new class of androgen-
repressed genes and insight into their pairwise control.";
J. Biol. Chem. 267:2303-2310(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                         SEQUENCE OF 8-17; 23-74 AND 414-4
MEDLINE-96220159; PubMed-8660345;
                                                                                                                                                                                                                                                                                                                      "Cloning and characterization of a rat prostatic epithelium.";
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                                                                                                                                                                                                                                                                                                         Chung-Kuo I Hsueh
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s SWISS-PROT entry is copyright. It is produced through a collaboratio ween the Swiss institute of Bioinformatics and the EMBL outstation European Bioinformatics institute. There are no restrictions on it by non-profit institutions as long as its content is in no wa
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1; Mismatches
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Sciurognathi; Muridae;
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01-JAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LY)
T1/LEU-1) (LYMPHOCYTE ANTIGEN CNE.)
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01-JAN-1988
01-JAN-1988
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Calvo J., Sole J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-87014786; PubMed-3093892;
Jones N.H., Clabby M.L., Dialynas D.P.,
Herzenberg L.A., Strominger J.L.;
"Isolation of complementary DNA clones
glycoprotein Tl/Leu-l.";
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Mammalia; Eutheria;
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PHOSPHORYLATION (BY SIMILARITY).
C4DD2FE25CB2C18B CRC64;
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Best Local S
Matches 5
SEQUENCE FROM A....
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Tomihama T., Shoji K., Hanyu H., Okano T.;
Tomihama T., Shoji K., Hanyu H., Okano T.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
-I- FUNCTION: RESPONSIBLE FOR THE CORE HISTONES (H2A, H2B, H3 AND H4).

THE N.TERMIMAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
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15-JUL-1998 (Rel. 36,
20-AUG-2001 (Rel. 40,
HISTONE DEACETYLASE (
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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3; X89400; CAA61584.2; J
4, AJ237927; CAA61584.2; J
4, AJ237929; CAA61584.2; J
4, AJ237930; CAA61584.2; J
4, AJ237931; CAA61584.2; J
4, AJ237931; CAA61584.2; J
4, AJ237932; CAA61584.2; J
4, AJ237932; CAA61584.2; J
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DATABASE: NA
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                                                                                                                                  Rosidae;
                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 32
USP_DROME
ID USP_DROME
ID USP_DROME
ID USP_DROME
ID USP O1-FEE
DT 20-AU
DE ULTRA
GN USP O
OS Droso
OC Eukar
OC Pter;
OC Ephy;
OC
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CANTON-S;
STRAIN-CANTON-S;
MEDLINE-90332404; PubMed-2165589;
MEDLINE-90332404; PubMed-2165589;
Henrich V.C., Sliter T.J., Lubahn D.B., Macintyre A., Gilbert L.I.;
"A steroid/thyroid hormone receptor superfamily member in Drosophila"
"A steroid/thyroid hormone receptor superfamily member in Drosophila"
"A steroid/thyroid hormone receptor superfamily member in Drosophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Me
Pterygota; Ne
Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USP_DROME STANDARD; PRT; 508 AA. P20153; Q9W535; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ULTRASPIRACLE PROTEIN (XR2C) (CHORION FACTOR USP OR NR2B4 OR CF1 OR EG:22E5 1 OR CG4380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
       MEDLINE-20196011; PubMed-10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Demailles J., Cadieu
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkov
Minana B., Kafatos F.C., Louis C., Siden-Riamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90384571; PubMed-2169594;
Oro A.E., McKeown M., Evans R.M.;
"Relationship between the product
locus and the vertebrate retinoid
Nature 347:298-301(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster that shares mammalian homologue.";
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PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF014824; AAB66486.1; -.
                                                                                                                                                                                                                                                                    STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATION, CELL CYCLE SIMILARITY).
SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY. HD SUBFAMILY 1.
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0850; Hist_deacetyl; 1.
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Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                         18:4143-4148(1990).
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Pred. No. 2.8e
1; Mismatches
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DOMAIN

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RX MEDLINE—2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Baradon R.C., Rogers Y.H.C., Blaze) R.G., Champe M., Pfeiffer B.D., Ra Randon R.C., Rogers Y.H.C., Blaze) R.G., Champe M., Pfeiffer B.D., Ra Baradon R.C., Baxter E.G., Halt G., Nelson C.R., Miklos G.L.G., Ra Wan K.H., Doyle C., Baxter E.G., Halt G., Nelson C.R., Miklos G.L.G., Ra Wan K.H., Doyle C., Baxter E.G., Halt G., Nelson C.R., Miklos G.L.G., Ra Ballew R.M., Basu A., Baxendaie J., Bayraktaroglu L., Beasley E.M., Den C.R., Mayraktaroglu L., Beasley E.M., Pfeiffer B.D., Botchian M.R., Bouck J., Brokstein P., Brottier P., Ra Burtis K.G., Busam D.A., Butler H., Godieu E., Center A., Chandra I., Ra Gartier J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.G., Busam D.A., Butler H., Godieu E., Center A., Chandra I., Posler G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Matsko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Mathel B., McIntosh T.C., McLeod M.P., McPherson D.L., Ra Kimmel B.E., Kulphy B., Murphy B., Murphy L., Muzzuy D.M., Nelson D.L., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Merkilov G., Milshina N.V., Mobarry C., Worts J., Nelson D.L., Nelson D.L., Nelson S., Sanders R.D.C., Scheeler F., Shen H., Ra Sher E., Shen H., Shari Y., Packer J.S., Zhan M., Zhang G., Zhao Q.
                                                                                                                                                                                   MEDLINE=94067348; Pubh
Yao T.-P., Froman B.M.
McKeown M.M., Cherbas
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                                                                                                                                                                                                                                                                                                       MEDLINE-91007257; PubMed-2120114;
Shea M.J., King D.L., Conboy M.J., Mariani B.D., Kafatos F.C.;
"Proteins that bind to Drosophila chorion cis-regulatory elements: a
new C2H2 zinc finger protein and a C2C2 steroid receptor-like
                                                                                                                                                                                                                                               SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.";
Science 287:2220-2222(2000).
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                                                                                                                               Nature
                                                                                                                                                                    "Functional
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(ECRES) SUCH AS IN THE PROMOTER SUBURIT: HETERODIMER OF USP AND CAPABLE OF HIGH-AFFINITY BINDING SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                               FUNCTION:
                                                    FUNCTION: RECEPTOR FOR ECDYSONE. MAY BE AN IMPORTANT MODULATOR INSECT METAMORPHOSIS. PLAYS AN IMPORTANT PART IN EMBRYONIC AND POST-EMBRYONIC DEVELOPMENT. BINDS TO ECDYSONE RESPONSE ELEMENTS. (ECRES) SUCH AS IN THE PROMOTER REGION OF S15 CHORION GENE.
                                                                                                                               366:476-479(1993)
                                                                                                                                                                                                                                                                                                                                                                                                             OF 15-294 FROM N.A.
                                                                                                                                                                                                                                                                              4:1128-1140(1990).
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                   HIGH-AFFINITY BINDING
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                                                                                                                                                                                   B.M., Jiang Z.,
rbas P., Evans R.
                                                                                                                                                                                                                      PubMed=8247157;
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                                                                                                                                                                  the
                                                                                                                                                                                   Cherbas
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RESULT 33
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ID P69_MYCHM
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OS Mycop
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EMBL; X52591; CAA56827.1; -.
EMBL; X52591; CAA56827.1; -.
EMBL; AL031765; CAA21122.1; -.
EMBL; AE003422; AAF45707.1; -.
EMBL; X53379; CAA37459.1; -.
PIR; A53672; A35872.
PIR; S11513; S11513.
PIR; S13119; S13119.
PIR; S13119; S13119.
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SEQUENCE FROM N.A. MEDLINE-89091146; PDudler R., Schmidha Schmidt T.;
                                                                                                         P69_MYCHR STANDARD; PRT;
P13362;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequenc
01-NOV-1997 (Rel. 35, Last annotat
TRANSPORT SYSTEM PERMEASE PROTEIN
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InterPro; IPR001723; Strdhormone_rcptor.
InterPro; IPR001628; zf-c4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-c4; 1.
PRINTS; PR00047; STROLDFINGER.
PRINTS; PR00398; STRDHORMONER.
                                                          Mycoplasmataceae;
NCBI_TaxID=2100;
                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                              Mycoplasma hyorhinis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
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| GSVGGS
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SM00399; ZnF_C4;
E; PS00031; NUCLE;
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MEASE PROTEIN P69.
            C.,
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tute of Bioinformatics
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G -> E (IN REF. 2).
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Pred. No. 2.8e+02;
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            7. Σ.
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RECEPTOR-TYPE.
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           Wettenhall R.E.
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use
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between the Swiss Institute of Bioinformatics
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Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti;
                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
THREAD BIOPOLYMER FILAMENT ALPHA SUBUNIT.
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                                                                                                                                                                  TISSUE-Slime gland;
MEDLINE-95213315; P
                                                                                                                                                                                                         SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                          Myxinidae; Eptatretinae; NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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S01830; S01830.
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                              SEQUENCE OF 1-383 FROM N.A. MEDLINE-98008138; PubMed-9345057; MEDLINE-98008138; PubMed-9345057; Hillion J. Le Coniat M., Jonveaux P., Berger R., Bernard O.A.; "AF6q21, a novel partner of the MLL gene in t(6:11)(q21:q23), d a forkhead transcriptional factor subfamily."; Blood 90:3714-3719(1997).

-I- FUNCTION: PROBABLE TRANSCRIPTION FACTOR THAT MAY TRIGGERS
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                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=98140118; Pubmed=9479491;
                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                       FOXO3A OR FKHRLL.
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                                                                                                                                                  Anderson
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                                                                                                                                                                                                                                                                                                                                                                       68 GSVGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
SUBCELLULAR LOCATION: NUCLEAR.
         FOR CELL DEATH
                     APOPTOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
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5; Conser
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                                                                                                                  M.J., Viars C.S., Czekay S., C;
and characterization of three I
an FKHR-like gene subfamily.";
47:187-199(1998).
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                                                                                                                                                                                                      Eutheria;
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Last annotation update)
(FORKHEAD IN RHABDOMYOSARCOMA-LIKE
                    TRANSCRIPTION FACTOR ING THE EXPRESSION OF
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COIL 2B.
POLY-GLY.
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Pred. No. 3.6e+02;
                                                                                                                                                                                                        Craniata; Vertebrata;
Catarrhini; Hominidae
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                                                                                                                                        human
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                     GENES
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FATA_VIBAN STANDARD; PRT; 726 AA.

AC P11461; P19830;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
EERRIC ANGUIBACTIN RECEPTOR PRECURSOR (OM2).
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Best Local S
Matches 5
Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
"Genetic and molecular characterization of essential components the Vibrio anguillarum plasmid-mediated iron-transport system.", Biol. Chem. 263:2853-2860(1988).
                                                                                                     MEDLINE=88139336; PubMed=2830268;
                                                                                                                                                                                                                                            Plasmid pJM1.
Bacteria; Pro
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SEQUENCE
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                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                  Bacteria; Proteobacteria; NCBI_TaxID=55601;
                                                                                                                                                                                                                                                                                        Vibrio anguillarum
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SMART; SM00339; FH; I.

PROSITE: PS00659; FORK_HEAD_1;

PROSITE: PS00659; FORK_HEAD_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF032886; AAC39592.1; -. EMBL; AJ001589; CAA04860.1; -. EMBL; AJ001590; CAA04861.1; -.
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MIM; 602681; -.
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nes 5; Conser
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PTM: PHOSPHORYLATED BY AKT1.
DISEASE: INVOLVED IN A T(6:11)(Q21;Q23) CHROMOSOMAL TRANSLOCATION
IN SECONDARY ACUTE LEUKEMIA THAT INVOLVES FOXO3A AND MLL.
SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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253 253
271 271
292 330
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Proto-oncogene; Phosphorylation.
AWGNLSYA -> WGKPVYS (IN REF. 2).
PDGGKSGKA -> LMGEERKT (IN REF. 2).
S -> T (IN REF. 2).
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P -> R (IN REF. 2).
D -> E (IN REF. 2).
LT -> AD (IN REF. 2).
W; E5B4E830665A9982 CRC64;
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Pred. No. 3.8e
1; Mismatches
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MISSING (IN REF. 2).
PGSPTSRSSDELDAWTDERSRINSNASTVSGRLSPIMAS
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PIGR_RABIT
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                                                                                                                                                                                                MEDLINE=84142246; PubMed=6322002;
Mostov K.E., Friedlander M., Blobel G.;
"The receptor for transepithelial transport of IgA and IgM contains
multiple immunoglobulin-like domains.";
Nature 308:37-43(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
POLYMERIC-IMMUNOGLOBULIN RECEPTOR PRECURSOR (POLY-IG RECEPTOR) (PIGR)
[CONTAINS: SECRETORY COMPONENT].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIGR_RABIT P01832;
                                               SEQUENCE OF 87-114 AND 410-428.
MEDLINE-88228032; PubMed-3131339;
Frutiger S., Hughes G.J., Hanly W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

Signal; Receptor; Transmembrane; Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03529; AAA91581.1; -. EMBL; M34504; AAA79859.1; -. PIR; B29928; B29928; PIR; PQ0051; PQ0051. InterPro; IPR()0531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986
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SEQUENCE
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MEDLINE-90185247; PubMed-2311935;
Farrell D.H., Mikesell P., Actis L.A., Crosa J.H.;
"A regulatory gene, angR, of the iron uptake system of Vibrio
"A regulatory gene, angr, of the join uptake system of Vibrio and regulation by in the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
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-1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
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   r S., Hughes G.J., Hanly secretory components of
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Pred.
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TONB C-TERMINAL BOX.
; 88B67A219395B154 CRC64;
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W.C., Jaton J.-C.;
different allotypes
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RESULT 38
FOX2_YEAST
ID FOX2_Y
AC Q02207
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DT 01-JUL
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Q02207;
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01-JUL-1993 (Rel. :
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carbohydrate content and their sites of N-linked glycosylation.";

J. Biol. Chem. 263:8120-8125(1998).

-i- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGN AT THE BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.

DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE TRANSMEMBRANE SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00410; IG; 5.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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PIR; A28077;
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nes 5; Conser
                                                                                                          1 GSLGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO SECRETED POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF ALLOTYPE T62. SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                      GNLGGS
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IPR003006; Ig_MHC.
IPR003600; Ig_like.
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N-LINKED (GLCNAC. . .); IN

(PARTIAL) AND T63.

N-LINKED (GLCNAC. . .)

(PARTIAL) AND T61).

K -> N (IN ALLOTYPE T61).

D -> E (IN ALLOTYPE T61).
sequence update)
                                                                                                                              Score 27; DB
Pred. No. 4.3e
1; Mismatches
                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE V-TYPE DOMAIN 2.
IG-LIKE V-TYPE DOMAIN 3.
IG-LIKE V-TYPE DOMAIN 4.
IG-LIKE V-TYPE DOMAIN 5.
POTENTIAL.
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DF2C44D2F1193C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          POLYMERIC-IMMUNOGLOBULIN RECEPTOR SECRETORY COMPONENT.
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-92202210; PubMed-1551874;
Hiltunen J.K., Wenzel B., Beyer A., Erdmann
"Peroxisomal multifunctional beta-oxidation
"Peroxisomal multifunctional beta-oxidation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duesterhoeft A., Philippsen P.; 'PNA sequencing and analysis of a 24.7 kb sequentromere CENII of Saccharomyces cerevisiae unknown open reading frames."; Yeast 8:749-759(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP: P25529; 1AHH.
SGD: S0001717; FOX2.
InterPro: IPR002198; ADH_short.
InterPro: IPR002347; Adh_short_C2.
InterPro: IPR002539; MacC_dehydratas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M86456; AAA34779.1; -.
EMBL; X65124; CAA46243.1; -.
EMBL; Z28234; CAA82079.1; -.
PIR: S25322; S25322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae. Molecular analysis of the J. Biol. Chem. 267:6646-6653(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C;
MEDLINE-93070612; PubMed-1441752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomyceta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE (EC 4.2.1.-); D-3-HYDROXYACYL COA DEHYDROGENASE (EC 1.1.1.-)]. FOX2 OR YKR009C OR YK108.
                                                                                                                                                                                                                                                                        PROSITE; PS00061; ADH_SHORT; 2.
PROSITE; PS00342; MICROBODIES_CTER; 1.
Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00106; adh_short; 2.
Pfam; PF01575; MaoC_dehydratas; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00080; SDRFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
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PATHWAY: BETA-OXIDATION PATHWAY:
PATHWAY: BETA-OXIDATION PATHWAY:
SUBCELLULAR LOCATION: PEROXISOMAL.
DOMAIN: CONTAINS TWO SOR DOMAINS.
SIMILARITY: BELONGS TO THE SHORT-CUATT.

SUBCILLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                            Isomerase;
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230 SHORT-CHA
230 SHORT-CHA
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469 BY SIMILA
469 BY SIMILA
AA; 98703 MW; 66FFDDD
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                                                                                          NAD (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                        MICROBODY TARGETING
                                                                                                                                                                                    SHORT-CHAIN DEHYDROGENASE LIKE SHORT-CHAIN DEHYDROGENASE LIKE
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      AD (BY SIMILARITY). SIMILARITY. 66FFD0D49C673788 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n R., Fossa A., Kunau W.H.
n protein of Saccharomyces
gene and gene product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HDE) (MULTIFUNCTIONAL
         CRC64;
                                                                                                                                                        SIGNAL
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DOMAIN
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-I- PTM: THE N-TERMINUS IS BLOCKED.
-I- PTM: TARGET FOR COAT-ASSOCIATED CASEIN
-I- SIMILARITY: CONTAINS 1 TENSIN DOMAIN.
-I- SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
PROSITE: PS50056; TYR_PHOSPHATASE_2; UNKNOWN_1.
PROSITE: PS00636; DNAJ_1; FALSE_NEG.
PROSITE: PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUR. J. BIOCHEM. 240:47, VVILLE, CHAIN AND
-1- FUNCTION: BINDS CLATHRIN HEAVY CHAIN AND
INTO REGULAR CAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00226; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U09237; AAA79037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              auxilin and its expression in bacteria.";
Eur. J. Biochem. 228:297-304(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
Bovidae; Bovinae; Bo
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001623; InterPro; IPR000387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Primary structure of the neuronal clathrin-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schroeder S., Morris S.A., Knorr R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95220355; PubMed-7705342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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Q27974;
680 GTLGGS 685
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910 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Outer membrane; Transport; TonB box; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U17281; AAA75311.1; -
InterPro; IPR000531; TonB_boxC.
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Elkins C., Chen C.J., Thomas C.E.;
"Characterization of the hgbA locus encoding a hemoglobin receptor
from Haemophilus ducreyi.";
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FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN
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B81505
C86590
H71600
JC5649
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hypothetical prote hypothetical prote

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C;Species: Bacilius subtills
C;Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 20-Jun-2000
C;Accession: S39671; G70050
R;Glaser; P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.;
A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Start codon: C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-281 <MAY>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-107 <KAW>
A; Cross references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79751.1; PID:g5104436
A; Cross references: Strain K1
          A;Title:
                                                                                                                                           N; Alternate names: protein ipa-16d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptomyces glaucescens
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-Dec-1999
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Best Local Similarity
6; Conserve
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyd A;Reference number: A72450; MUID:99310339
A;Accession: G72668
                                                                                                                                                            phosphotransferase system enzyme II homolog ywbA - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S44230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references:
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63 GSLGGS 68
                                                                                                                                                                                                                                                                            91 GSLGGS
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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    Streptomyces glaucescens

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                                                         Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.;
                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No.
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A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrarl, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Llu, H.; Masuda, S.; Mau Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                     A;Gene: ywbA
C;Superfamily: phosphotransferase system
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X73124; NID:g413923; PIDN:CAA51572.1; PID:g413940
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
R;Kunst, F.; Ogasawara N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 340, 246-256, 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-444 <GLA>
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A;Accession: S39671
232 GSLGGS
                                                                 1 GSLGGS 6
                                                                                                                                  Conservative
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Pred. No. 1.2
0; Mismatches
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1.2e+02;
0;
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N; Alternate names: probable cellobiose phosphotransferase enzyme
                                                   PTS lichenan-specific enzyme IIC component licC - Bacillus subtilis
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C:;Beccies: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: F69651; S57760
R:Kunst, F:, Ogasawara, N:, Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A.; Althors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Riotla, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sekeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Capuania, S.; Scoffone, F.; Scoffone, F.; Scoffone, F.; Scoffone, F.; Scoffone, M.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
A. *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-positive bacterium Bacillus subtili a.* *Ctaffine 'rerolation' acid accusence of the Gram-p

A; Molecule type: DNA A; Residues: 1-452 <KUN> A; Status: preliminary; nucleic acid sequence not shown; translation not

A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15884.1; PID:g26363 A;Experimental source: strain 168

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A;Status: preliminary
A;Molecule type: DNA
A;Moslecule type: DNA
A;Residues: 1-935 <SCH>
A;Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.260
A;Experimental source: cosmid contig 13E11; strain 74
C;Genetics:
                                                                                                                                                                                     hypothetical protein 13E11.260 [imported] - Neurospora crassa C;Speckes: Neurospora crassa C;Speckes: Neurospora crassa C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000 C;Accession: T48778
                                                                                                                                                                                                                                                               RESULT
T48778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor C;Keywords: iron transport; membrane protein; metal binding; receptor F;1-22/Domain: signal sequence #status predicted <SIG>
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R;Daban, M.; Medrano, A.; Querol, E.
Biochem. J. 315, 257-264, 1996
A;Title: Cloning, sequencing and expression
A;Reference number: $66574; MUID:96207589
A;Accession: $66574
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A;Accession: S57760
                                                                                                                                                 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, submitted to the Protein Sequence Database, App
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A; Residues: 1-452 <GLA>
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                                                                                                            A; Reference number: Z24541
A; Accession: T48778
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A;Residues: 1-931 <DAB>
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Pred. No. 2.4e+02;
Pred. No. 2.4e+02;
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Pred. No. 1.2e+02;
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                                                                                                                                                 it, P.; Fartmann, B.; Holland, R.;
April 2000
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A; Residues: 1-936 < WHI>
A; Cross references: GB; AE001826;
A; Cross references: Strain R1
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                                                                                                                                                                                                                                                                                A;Reference number: 225858
A;Accession: T51904
A;Starue:
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T51904
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A; Map position: 6
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                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                     R;Schulte, U.;
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Best Local
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6; Conserv
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C;Accession: F75622
C;Acce
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A; Residues: 1-1051 <SCH>
A; Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23I11.160
A; Cross-references: BAC clone B23I11; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein B23111.160 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A;Map position: 2
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                                        Score 30; DB 2;
Pred. No. 2.8e+02;
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
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August 2000
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                                                                                                   Length 1051;
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luteinizing hormone beta-subunit - quail
c; Species: Coturnix coturnix (quail)
c; Species: Coturnix coturnix (quail)
c; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C; Accession: I51242
R; Ando, H; Ishil, S.
Gen. Comp. Endocrinol. 93, 357-368, 1994
A; Title: Molecular cloning of complementary deoxyribonucleic acids for the lurnix coturnix japonica).
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A;Gene: STPK1
A;Map position: 1
C;Superfamily: Leishmanla major probable membrane
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A;Residues: 1-1557 <PYL>
A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24682.1; PID:g3002481; GSPDB:GN00
A;Experimental source: strain MHOM/IL/81/Friedlin
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A;Gene:
    A; Reference
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 08-Feb-1996
C;Accession: A57376
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A;Accession: A57376
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Mol. Cell. Biol. 1
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A; Residues: 1-1346 <LIN>
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Matches 6
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Best Local Similarity
Matches 6; Conserv
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960 GSLGGS
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I51241; MUID:94252550
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Pred. No. 4.1e+02;
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Pred. No. 3.5e+02;
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S44225
strf protein - Streptomyces bluensis (fragment)
C:Species: Streptomyces bluensis
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997
C:Accession: S44225
R:Mayer, G.: Piepersberg, W.
R:Mayer, G.: Piepersberg, W.
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                                                                                                                                   A;Start codon:
C;Superfamily:
                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-267 <MAY>
                                                                                                                                                                                                                              A; Reference number: A; Accession: $44225
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Best Local Similarity
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-166 <AND>
A;Residues: 1-166 <AND>
A;Cross=references: GB:S70834; NID:g546921; PIDN:AAB30867.1; PID:g546922
C;Superfamily: pituitary glycoprotein hormone beta chain
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A; Note: F8F6.160
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A;Experimental source: cultivar Columbia; BAC
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A; Residues: 1-252 <BEV>
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A; Accession: T48422
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R; Bevan, M.;
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T48422
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Best Local s
Matches 5
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91 GSIGGS
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                           GSLGGS 6
                                                         Similarity
5; Conserv
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5; Conser
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Streptomyces strf protein
96
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                               EMBL: X78972;
                                                                    93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van Staveren, M.;
                                                       Score 28; DB
Pred. No. 1.8e
1; Mismatches
                                                                                                                                                                               NID:g475227; PIDN:CAA55568.1; PID:g581604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB
Pred. No. 1.7e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB
Pred. No. 1.16
1; Mismatches
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                                                                                                                                                                                                                                                          April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
1.7e+02;
0;
                                                                      DB 2;
1.8e+02;
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1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Dirkse, W.; Stiekema, W.; Bancroft, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone
                                                       0.
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                                                                                    Length 267
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                                                       Indels
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A;Cross-references: EMBL:AC0042
C;Genetics:
A;Map position: 1
A;Introns: 48/1; 155/3; 365/3
A;Note: T14N5.7
C;Superfamily: glucose transpor
C;Keywords: sugar transport; tr
RESULT
E72608
                                                                                                                                                                                                                                                                                                                                                                                                              probable monosaccharidé transport protein T14N5.7 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 24-Sep-1999 C;Accession: T00450 R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W. submitted to the EMBL Data Library, September 1998 A;Reference number: 214152 A;Recession: T00450
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                                                                                                                                                                                                                                                                                                                                                            A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-504 <FED>
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A;Cross-references: FlyBase:FBgn0003130
C;Superfamily: paired box transcription factor
F;5-130/Domain: paired box homology <PBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M86927; NID:g158155; PID:g158156
A;Note: Sequence extracted from NCBI backbone (NCBIN:90907,
R;Bopp, D; Jamet, E.; Baumgartner, S.; Burri, M.; Noll, M.
BMBO J. 8, 3447-3457, 1989
A;Title: Isolation of two tissue-specific Drosophila paired
A;Reference number: S06950; MUID:90059940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 69, 159-172, 1992
A:Title: The paired box gene pox neuro: a A:Reference number: A38153; MUID:92208941
A:Accession: A38153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Drosophila melanogaster C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 C:Accession: A38153; S06951 R:Dambly-Chaudiere, C.; Jamet, E.; Burri, M.; Bopp, Cell 69, 159-172, 1992
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A38153
paired
C; Speci
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A;Residues: 1-135 <BOP>
A;Cross-references: EMBL:X58917; NID:g8360; PIDN:CAA41721.1; PID:g1405550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
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Best Local S
Matches 5
                                                                                                                                                                                                                            ;Superfamily: glucose transport protein
;Keywords: sugar transport; transmembra
                                                                                                                                                               Query Match
Best Local
                                                                                                                                            Matches
                                                                      33
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nes 5; Conserv
                 16
                                                                                         1 GSLGGS 6
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                                                                      GSMGGS
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                                                                                                                                                           83.3¢
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                                                                                                                                                                                                                               transmembrane
                                                                                                                                                       Score 28;
Pred. No.
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                          NID:g3176694;
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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. 3.4e+02;
. ~ 0;
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                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bopp, D.; Basler, K.; Hafen, E.; Dumont,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pax-8;
                                                                                                                                                                                                                                                                                                                                      PIDN: AAC34349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 425
                                                                                                                                                                        Length 504
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C83527
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C;Accession: C83527
C;Accession: C83527
R;Stover, C.K.; Pham, X.Q.; Erwin, Adman, S.; Yuan, Y.; Brody, L.L.; C
LOIY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337 A;Accession: C83527
                                                                                                                                                                                prolyl-tRNA synthetase PA0956 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: At2gubb/
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Sequence and analysis of chromosome A; Reference number: A84420; MUID: 20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; M.; Koo, H.; Moffat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutator-like transposase [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80323.1; PID:g5105009 A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E72608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-562 <KAW>
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C;Species: Aeropyrum pernix
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Best Local S
Matches 5
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Map position: 2
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.Oo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter e 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                           165 GSIGGS
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5; Conserv
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%;
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                                                                                                                   Coulter, S.N.; Fo
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Pred. No. 3.8e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; L., 3.8e+02; 0;
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                                                                                                                hi, S.D.;
Folger, K
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K.R.; Kas,
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                                            an opportunistic
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Larbig,
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C;Species: Escherichia coli
C;Date: 30-Sep-1992 *sequence_revision 31-Oct-1997 *text_change 24-Sep-1999
C;Accession: B64744; JV0110; JV0061
C;Accession: B64744; JV0110; JV0061
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Accession: B64744
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-126, 'HV', 129-204, 'RPLTNSRCWRR', 217-515, 'RA' <ZHO>
A; Residues: GB: M32357; NID: g145802; PIDN: AAA23710.1; PID: g145803
A: Cross-references: GB: M32357; NID: g145802; PIDN: AAA23710.1; PID: g145803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-25,'IV', 28-204,'Q',206-572 <ERI>
A; Residues: 1-25,'IV', 28-204,'Q',206-572 <ERI>
A; Cross-references: GB:M97858; NID:g147361; PIDN:AAA24420.1; PID:g147362
A; Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in R; Zhou, Z.; Syvanen, M.
J. Bacteriol. 172, 281-286, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000128; GB:U00096; NID:g1786383; PIDN:AAC73305.1; A;Experimental source: strain K-12, substrain MG1655 R;Eriani, G.; Delarue, M.; Poch, O.; Gangloff, J.; Moras, D. Nature 347, 203-206, 1990 A;Title: Partition of trNA synthetases into two classes based on mutually & A;Reference number: JV0110; MUID:90370122
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C;Superfamily: proline--tRNA ligase
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A;Molecule type: DNA
A;Residues: 1-571 <STO>
A;Cross-references: GB:AE004529; GB:AE004091; NID:g9946851; PIDN:AAG04345.1; GSPDB:GN001
RESULT
C64089
                                                                                                                                                                                                                                                                                     C; Superfamily: proline--tRNA ligase
C; Keywords: aminoacyl-tRNA synthetase;
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N;Alternate names: global RNA synthesis factor; prolyl-tRNA synthetase
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A; Map position:
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1; Mismatches
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                                                                                    hypothetical protein Opa - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 17-Nov-2000 C;Accession: T08600
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A; Reference number: Z16450
A; Accession: T08600
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                                             submitted to the EMBL Data Library, August
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200 GSIGGS 205

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R.A.; Friedman, T.B.;

Smith, B.;

Wallrath,

L.L.; Johnson,

S.; Burnett,

J.B.

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proline--trna ligase (EC 6.1.1.15) - Haemophilus influenzae (strain N;Alternate names: proly1-trna synthetase C;Species: Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-J C;Accession: C64089
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                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: D85504
                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: D85504
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             proline tRNA synthetase [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli (C;Date: 16:Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar
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C; Keywords: aminoacyl-tRNA synthetase;
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A;Accession: C64089
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C; Superfamily:
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A; Residues: 1-572 <STO>
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Nature 409, 529-533, 2001
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A; Residues: 1-572 <TIGR>
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                                     Score 28; DB 2;
Pred. No. 3.8e+02;
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Glodek, A.; Kelley, J.M.; Weidman
Fuhrmann, J.L.; Geoghagen, N.S.M.
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C;Accession: G95559
R;Theologis, A,; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Saliberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Creature, nealtminary
A;Cross-references: GB:AE005173; NID:g4220448; PIDN:AAD12675.1; GSPDB:GN00141 C;Genetics:
                                        A; Molecule type: DNA
A; Residues: 1-729 <STO>
                                                             A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F5F19.7 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
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A:Map position: 3
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N;Alternate names: protein T5C2.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47378
R;Obermaler, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; 1
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24463
A;Accession: T47378
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A; Residues: 1-675 <0
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A;Molecule type: mRNA
A;Residues: 1-654 <WAGO
A;Cross-references: EMBL:AF018078; NID:g2394383; PI
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. 4.5e+02;
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; Maiti, R.;
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                                                                                                                                                                                H.; Tallon,
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A; Molecule type: DNA
A; Residues: 1-758 < DNA
A; Residues: 1-758 < DNA
A; Cross-references: EMBL: Z28034; NID: g486043; PIDN: CAA881869.1; PID: g486044;
A; Experimental source: strain S288C
R; Purnelle, B.; Skala, J.; van Dyck, L.; Goffeau, A.
Yeast 10, 125-130, 1994
A; Title: Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new gulator ABF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: B86403
                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: hypothetical protein YKL034w precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YKL247
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Sep-2000
C;Accession: S37855; S41670; S36853
A; Molecule type: DNA
A; Residues: 1-758 < PU2>
                                                                  A; Reference number: S41667; A; Accession: S41670
                                                                                                                                                                                                                                                                                                                            R; Purnelle, B.; Skala, J.; van Dyck, L.; Tettelin, H.; submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B86403
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.;
                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S37855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                        A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-749 <STO>
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar_2001 *sequence_revision 02-Mar_2001 *text_change 31-Mar-2001
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A; Map position:
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conser
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83
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83.3%;
                                                                                         MUID: 94262309
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Pred. No. 5e+(
1; Mismatches
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Pred. No. 4.9e
1; Mismatches
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tches 0;
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5e+02;
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                                                                                                                                                                                                                                                                                                                                                          Goffeau,
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Maiti, R.; Marzia
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C/Superfamily: Saccharomyces cerevisiae hypothetical protein C/Keywords: transmembrane protein F:1-26/Domain: signal sequence #status predicted <SIG>F:27-758/Product: hypothetical protein YKL034w #status predicted: hypothetical protein YKL034w #status predicted <TM1>F:400-416/Domain: transmembrane #status predicted <TM2>F:400-45/Domain: transmembrane #status predicted <TM3>F:461-477/Domain: transmembrane #status predicted <TM3>F:528-544/Domain: transmembrane #status predicted <TM5>F:538-554/Domain: transmembrane #status predicted <TM5>F:607-623/Domain: transmembrane #status predicted <TM5>F:638-554/Domain: transmembrane #status predicted <TM5>F:638-554/Domain: transmembrane #status predicted <TM5>F:638-554/Domain: transmembrane #status predicted <TM5>F:638-554/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable heme utilization protein precursor PA1302 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A83484
hypothetical protein F7N22.13 - Arabidopsis thallana C:Species: Arabidopsis thallana (mouse-ear cress) C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Aug-2000 C:Accession: T01168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
A;Accession: A83484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Residues: 1-570 < PU3>
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A;Accession: S36853
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A;Title: The sequence of a 12 kb fragment on the left
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A; Gene: PAl
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A;Residues: 1-851 <570>
A;Cross-references: GB:AE004559; GB:AE004091; NID:g9947228; PIDN:AAG04691.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fo
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Matches 5
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                         668 GSIGGS
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nes 5; Conserv
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83.3%;
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; Pred. No. 5.1e
1; Mismatches
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Pred. No.
1; Mismatc
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5.7e+02;
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,.1e+02;
0;
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                                                                                                                                                                                                                                                                                                                             Length 851;
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                        RESULT
JE0291
FB19 protein -
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A; Introns: 60/1;
A; Introns: F7N22.13
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submitted to the EMBL Data Library, April 1
A; Description: The sequence of A. thaliana
A; Reference number: Z14250
A; Accession: T01168
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: Cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
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A;Cross-references: EMBL:AF058825; NID:g3047060; PID:g3047071
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487 A;Accession: E84521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, submitted to the EMBL Data Library, June 1998 A;Description: Arabidopsis thaliana chromosome A;Reference number: Z14680 A;Accession: T02597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutator-like transposase [imported] - Arabidopsis thallana N;Alternate names: hypothetical protein F26C4.7 C:Species: Arabidopsis thallana (mouse-ear cress) C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_c
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                                                                                                                                                                                 A;Map position: 2
A;Introns: 70/2; 151/1; 292/3; 420/3
C;Superfamily: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-895 <STO>
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A;Molecule type: DNA
A;Residues: 1-895 <ROU>
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                                                                                                                                                                                                                                             A;Gene: At2g14790; F26C24.7
                                                                                                                                                                                                                                                                                        A;Cross-references:
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129 GSIGGS 134
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5; Conserv
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5; Conser
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                                                                               Conservative
                                                                                                                                                                                                                                                                                      GB:AE002093; NID:g3252817; PIDN:AAC24187.1; GSPDB:GN00139
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                                                                                                 93.3%;
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Pred.
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Pred. No. 6e+02;
l; Mismatches
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5.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II BAC F26C24 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                             of the plant Arabidopsis thaliana
                                                                                                                                                                                     protein F26C24.7
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human

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probable mutator-like transposase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis discovery) Arabidopsis discovery) Arabidopsis discovery d
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A;Map po
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1028 <570>
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C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Accession: JE0291
R;Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto Biochem. Biophys. Res. Commun. 250, 555-557; 1998
A;Title: Cloning of a new gene (FB19) within HLA class I region.
A;Reference number: JE0291; MUID:99003493
A;Accession: JE0291
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E85089
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A; Residues: 1-940 <TOT>
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les 5; Conserv
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83.3%;
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83.3%;
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Pred. No.
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Pred. No. 6.3e+02;
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6.9e+02;
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; Dewar,
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RESULT
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T14270
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A; Residues: 1-1249 < KIM>
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T13958
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C;Accession: f14270
R;Kim, J.H.; Liao, D.; Lau, L.F.; Huganir, R.L.
Neuron 20, 683-691, 1998
A;Title: SynGAP: a synaptic RasGAP that associa
A;Reference number: Z17950; MUID:98240917
A;Accession: T14270
                                                                                                                                                                                                                                                           Ras-GTPase activating protein SynGAP-b - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Sep-1999 #sequence_revision 20-Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: mRNA
A:Residues: 1-1166 <SUZ>
A:Cross references: EMB1:AB016962; NID:d1261311; PID:d1038706; PIDN:CAB19493.1
A:Experimental source: strain Sprague Dawley
C:Genetics:
A:Gene: synGAP-b1
                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data
A;Description: SynGAP-b1.
A;Reference number: Z17834
A;Accession: T13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synGAP-bl protein - rat
C;Species: Rattus norvegicus (Norway ra
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1127 <STO>
A;Cross-references: GB:AE005172; NID:g11560180; PIDN:AAG38122.1; GSPDB:GN00141
C;GenetLcs:
A;Map position: 1
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                                                                                          EMBL: AF058790;
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83.3%;
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                                                                                                                                                                            RasGAP that associates with the MUID:98240917
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Score 28; DB 2; Le
Pred. No. 8.5e+02;
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Pred. No.
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Pred. No.
                                                                                  NID:g3722228; PID:g3722229;
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on 20-sep-1999
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7.9e+02,
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/.6e+02;
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                                                                                    PIDN: AAC63511.1
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C; Date:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ras GTPase-activating protein, synaptic - rac
N;Alternate names: protein SynGAP
C;Species: Rattus norvegicus (Norway rat)
                                                                                                            hypothetical protein YJL067w · yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRA116; hypothetical protein J1107
C;Species: Saccharomyces cerevision
C;Species: Saccharomyces cerevision
C;Accession: S50805; S47124; S56841
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyca, Reference number: S50798; MUID:95282514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable calcium-transporting ATPase - C:Species: Schizosaccharom....
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A; Residues: 1-1293 <CHE>
A; Cross-references: EMBL: AF048976; NID: 92935447; PID: 92935448; PIDN: AAC08071.1
A; Experimental source: strain Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1402 <0D2>
A;Cross-references: EMBL:Z67757; NID:g1061288; PIDN:CAA91777.1;
A;Experimental source: strain 972h-; cosmid c24B11
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A; Accession: T38339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: T38339; S62557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
A; Molecule type: DNA
A; Residues: 1-116 <VAN>
A; Cross-references: EMBL
A; Note: the nucleotide s
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A; Map position: 1L
A; Introns: 124/3
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                                                                                              A; Reference number: S50798; A; Accession: S50805
                                                                          A; Status: nucleic acid sequence not shown;
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Best Local S
Matches S
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Best Local
 Cross-references: EMBL: 234288; NID: 9498992; Note: the nucleotide sequence was submitted
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83.3%;
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Pred.
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Pred. No. 8.8e+02;
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   PIDN:CAA84056.1;
to the EMBL Data
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     PID:g499000
Library, June 1994
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                                                                                                                                     Saccharomyces cerevisia
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A; Molecule type: DNA
A; Residues: 1-116 < VAW>
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A; Residues: 1-116 < POH>
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R; Drolet, M.; Zanga,
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A; Residues: 1-149 < DRO>
         A;Status: preliminary;
A;Molecule type: DNA
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A;Cross-references: EMBL:Z34288; NID:g498992; PIDN:CAA84056.1; R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995 A;Reference number: S56835 A;Reference S56841
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              R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Kr. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, N. Ruture 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987

A;Accession: G70897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of trans
A;Reference number: S12188; MUID:91125140
A;Accession: S12192
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 5 - Thiobacillus C; Species: Thiobacillus ferrooxidans C; Date: 19-Mar-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Saccharomyces hypothetical protein YJL067w
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                                                                                                                                                                                                  hypothetical protein Rv1105 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-C;Accession: G70897
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nucleic
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83.3%;
  acid sequence
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Pred. No.
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Pred. No. 1.6e+02;
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    shown;
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RESULT 40
JE0045
imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Mar-2000
C;Accession: JE0045; S04399; S16798
R;Fanil, R; Bazzicalupo, M; Damiani, G.; Bianchi, A.; Schipani, C.; Sgaramella, V.; Pol
Mol. Gen. Genet. 216, 224-229, 1989
A;Title: Cloning of histidine genes of Azospirillum brasilense: organization of the ABFH
A;Reference number: JE0045; MUID:89313660
A;Residues: 1-207 c;RAN>
A;Residues: 1-207 c;RAN>
A;Cross-references: EMBL:X61207; NID:g38669; PIDN:CAA43515.1; PID:g38670
C;Genetics: A;Gene: hisB
C;Superfamily: imidazoleglycerol-phosphate dehydratase; imidazoleglycerol-phosphate dehy
C;Keywords: carbon-oxygen lyase; histidine biosynthesis; hydro-lyase
F;36-203/Domain: imidazoleglycerol-phosphate dehydratase homology <IPD>
Search completed: February 4, 2002, 08:00:55 Job time: 39 sec
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A;Cross-references: GB.AL021897; GB:AL123456; NID:g3256022; PIDN:CAA17221.1; PID:e12519; A;Experimental source: strain H37Rv
C;GenetLcs:
A;Gene: Rv1105
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Best Local Similarity 83.3
Matches 5; Conservative
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98 GNLGGS 103
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062766 rattus norv
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kk Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamaya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
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01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HYPOTHETICAL 11.4 KDA PROTEIN APE0773.
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                       MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., E.
Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                        Ephydroidea;
                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso
                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
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DNA Res. 6:83-101(1999).
                                                                                                STRAIN-BERKELEY;
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NCBI_TaxID=7227;
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RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dletz S.M.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Worris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Sunnders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X.,
RA Gibbs R.A., Zhong F.N., Zhong W., Zhon X., Zhu X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhong S., Zhu X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Zhong W., Zhong S., Zhu X., Smith H.O.,
RA Gibbs R.A., Shong F.N., Rubin G.M., Wenter J.C.;
DR EMBL, Accounce of Drosophila melanogaster.*;
Scheeler F., Spendling A.C., Scheeler F., Shon H., Wang A.H.,
Scheence 287:2185-2195(2000).
DR EMBL, Accounce of Drosophila melanogaster.*;
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Courses.";
J. Virol. 70:3589-3598(1996)
EMBL; U47563; AAB06904.1; -.
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Hutto C., Zhou Y., He J., Geffin R., Hill M., Scott W., Wood
"Longitudinal studies of viral sequence, viral phenotype, ar
immunologic parameters of human immunodeficiency virus type
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                                                                                                                                                        perinatally infected
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Q75018;
01-NOV-1996
01-NOV-1996
01-JUN-2001
  SEQUENCE FROM N.A. Mulenga A., Sugimoto Submitted (MAY-1998)
                                                                       Haemaphysalis longicornis.
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Parasitiformes; Ixodida; Ixodidae; Haemaphysalis.
NCBI_TaxID=44386;
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MEDLINE-96211491; PubMed-8648693;

Hutto C., Zhou Y., He J., Geffin R., Hill M., Scott W., Wood C.

"Longitudinal studies of viral sequence, viral phenotype, and immunologic parameters of human immunodeficiency virus type 1 infection in perinatally infected twins with discordant disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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EMBL; U47568; AAB06909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         courses.";
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NCBI_TaxID=11676;
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// iruses; Retroid viruses; Retroviridae;
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PF00516; GP120;
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001 (TrEMBLrel. 17, Last
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Q1-NOV-1998 (TrEMBLrel. 08
GLA Q GENES STRB1, STRF, S
STRF. STRPLOMES STRB1, STRF, S
Q9VBE0;
Q9VBE0;
01-MAY-2000
                                                                                                                                                                  STRAIN-ATCC 13032 (GLA.0);

MEDLINE-96204519; PubMed-8628239;

Beyer S., Distler J., Piepersberg W.;

"The str gene cluster for the biosynthesis of 5'-hydroxystreptomycin in Streptomyces glaucescens GLA.0 (ETH 22794): new operons and evidence for pathway-specific regulation by StrR.";

MO1. Gene Genet. 257-784 (1996).

EMBL; X78974; CAA55572.1; -.

EMBL; AJ006985; CAA07379.1; -.

EMBL; AJ006985; CAA07379.1; -.
                                                                                                                                                                                                                                                                                          Piepersberg W.;
"Streptomycin Production in Streptomycetes: a Progress Report.";
(In) Baltz R.H., Hegeman G.D., Skatrud P.L. (eds.);
Industrial microorganisms. Basic and applied molecular genetics,
pp.183-194, ASM Press, Herndon (1993).
                                                                                                                                                                                                                                                                                                                                                                                              Piepersberg W.;
Submitted (JUN-1000)
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Submitted
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STRAIN-ATCC 13032 (GLA.0);
STRAIN-ATCC 13032 (GLA.0);
Retzlaff L., Mayer G., Beyer
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Best Loc
Matches
                  Q9X6F4
Q9X6F4;
Q1-NOV-1999
Q1-NOV-1999
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, FIBRONECTIN-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel.
CG6478 PROTEIN.
CG6478.
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ilarity 100.
Conservative
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                                                                                         PRELIMINARY;
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Last annotation update)
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Pred. No. 1.7e+02;
; Mismatches 0;
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a; Brachycera;
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RESULT
Q9FGC2
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Q9FGC2;
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01-MAR-2001 (TremBI
01-JUN-2001 (TremBE
DNA HELICASE-LIKE
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09B0G1;
01-JUN-2001
01-JUN-2001
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"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
EMBL; AL136594; CAB66529.1; -.
                                                                                                                                                                                                       EMBL; AL136594; CAB66529.1;
Hypothetical protein.
SEQUENCE 590 AA; 63303 M
                                                                                                                                                                                                                                                                                                                                    TISSUE-AMYGDALA
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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DKFZP7610132.
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L 63.3 KDA PROTEIN.
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etazoa; Chordata;
theria; Primates;
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Pred.
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Pred. No. 4e+02;
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and collagen.";
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01-MAR-2001
Q9AV46
Q9AV46;
Q1-JUN-2001 (TrEMBLrel.
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Q9U193;
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STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzad
Smith D.F.;
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SEQUENCE
                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 7
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Rajandream M.A., Barrell
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                             "A physical map of the Leishmania Genome Res. 8:135-145(1998). EMBL; AL117319; CAB55519.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana (submitted (APR-1999) to the EMBL/GenBank/DDBJEMBL, AB026643; BAB09253.1; -
InterPro, IPR001410; DEAD.
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S.;
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hilarity 100.
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(TrEMBLrel. 16, Last annotation update)
78.7 KDA PROTEIN.
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Pred. No. 5.4
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"The csu locus of Vibrio parahaemolyticus.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF339087; AAK37523.1;
SEQUENCE 802 AA; 88127 MW; 653711976A2BF37A CRC64;
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBa0093B11 genomic sequence.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC024594; AAK21344.1; -.
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HYPOTHETICAL 86.7 KDA PROTEIN.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach-
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bacteria; Proteobacteria;
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Plasmid.
SEQUENCE
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EMBL; U16017; AAC43485.1; -.

Interpro; IPRO00531; TonB_boxC.

Pfam; PF00593; TonB_boxC. 1.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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Gonzalez G.C., Yu
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R.H., Rosteck P.R.
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TBP1 GENE PR
Q9P6Z0;
Q9P6Z0;
01-OCT-2000
01-OCT-2000
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Paban M., Medrano A., Querol E.;

"Cloning, sequencing and expression of the transferrin-binding protein
1 gene from Actinobacillus pleuropneumoniae.";

Biochem J. 315:257-264(1996).

EMBL; Z49708; CAA89810.1; -

InterPro; IPR000531; TonB_boxC.

Pfam; PF00593; TonB_boxC; 1.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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MEDLINE-96030198; vu R.H., Rosteck P.R. Jr., Schryvers A.B.
Gonzalez G.C., vu R.H., Rosteck P.R. Jr., Schryvers A.B.
Sequence, genetic analysis, and expression of Actinobac
Psequence, genetic analysis, and expression of Actinobac
pleuropneumoniae transferrin receptor genes.";
Microbiology 141:2405-2416(1995).
EMBL; U16019; AAC43487.1; -.
INTERPROJUSTITONB_DOXC.
Pfam; PF00593; TONB_DOXC: 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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MEDLINE-96207589; PubMed-8670116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                   151
                                                                                                                1 GSLGGS
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                                                                                                   GSLGGS
                                                                                                                                                 Similarity 6; Conserv
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23
931 AA;
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(TrEMBLrel.
                                                                                                                                                    Conservative
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931
106326
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 Created)
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Last annotation update)
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TBP1 GENE.
W; D777366E2FDA54F9 CRC64;
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Pred.
                                                                                                                                                                Score 30;
Pred. No.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                      PRT;
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                                                                                                                                                     Mismatches
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                                      935
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ches 0;
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on of Actinobacillus
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Pasteurellaceae;
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sequence update)

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RESULT
Q9RZS3
ID Q9
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Best Local S
Matches 6
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Best Local S
Matches 6
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InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; Zf-C2H2; 2.
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Zinc-finger. SEQUENCE 935 AA; 103980 MM; 35F0F645
                                                                                                                                                                                                                                                                                                          MEDLINE=20036896; PubMed=10567266; Mitte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                          PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
Hypothetical protein; Plasmid; Complete prot
SEQUENCE 936 AA; 97723 MW; 4A8D433D7F149
                                                                                                                                                                                                                    "Genome sequence of the radioresistant radiodurans R1.; Science 286:1571-1577(1999).
EMBL; AE001826; AAF12631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRB0041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HYPOTHETICAL 97.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurospora crassa.
Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Neu
NCBI_TaxID=5141;
                                                                                                                                                                                                    TIGR; DRB0041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid MP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                              InterPro; IPR002173; PfkB.
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    Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus/Deinococcus
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  100.
Milarity 100.
Conservative
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H.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ
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Score 30; DE Pred. No. 6.9; Mismatches
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group; Deinococcales;
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                                                                                                          Complete proteome 4A8D433D7F1495C0 /
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                                                                                                                                                                                                                                                                                      bacterium
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                                        Length 936;
                                                                                                            CRC64;
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                                                                                                                                                                                                                                                                                      Deinococcus
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Gaps
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RESULT 087296 ID 298 ID
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SEQUENCE FROM N.A.

STRAIN-H1689 TYPE B;
MEDLINE-98427137; PubMed-9746572;
Ren Z., Jin H., Morton D.J., Stull T.L.;
Infect. Inmun. 66:4733-4741(1998).
EMBL; AF022910; AAC60790.1; -.
InterPro; IPR001931; TonB_boxC.
InterPro; IPR001931; MITOCH_CARRIER; UNKNOWN_1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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Best Local
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O87296;
O1-NOV-1998 (TrEMBLrel. 0
O1-NOV-1998 (TREMBLrel. 0
O1-JUN-2001 (TREMBLREL. 1
HEMOGLOBIN BINDING PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cope L.D., Hrkal Z., Hansen E.J.;
Detection of Phase Variation in Expre
Hemoglobin and Hemoglobin-Haptoglobin
Haemophilus influenzae.";
Infect. Immun. 68:4092-4101(2000).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMOGLOBIN BINDING PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF221060; AAF80178.1; Interpro; IPR001993; Mitoch_carrier.Interpro; IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGPB.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
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800 GSLGGS
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PF00593; TOOB_boxC; 1.

PE; PS00215; MITOCH_CARRIER; UNKNOWN_1.

PE; PS01156; TONB_DEPENDENT_REC_2; 1.

PROCE 993 AA; 113616 MW; A551BF3B2C641612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local S
Matches
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Best Local
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SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
Amanatides P.G., Richards S., As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cope L.D., Hrkal Z., Hansen E.J.;
"Detection of Phase Variation in Expression of Proteins Involved Hemoglobin and Hemoglobin-Haptoglobin Binding by Nontypeable Infect. Immun. 68:4092-4101(2000).
EMBL; AP221059; AP80176.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTEFFIG. AFACTORIST DOXC; 1.
Pfam; PF00593; TONB_DOXC; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CG10042 PROTEIN. CG17393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VGA4
Q9VGA4;
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6; Conserv
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6; Conser
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Llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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, Last sequence up
, Last annotation
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081 AA
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                                                   Evans C.A.,
, Hoskins R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) DB 2;
) 7.6e+02;
0;
                                 Ashburner M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4e+02;
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                            R.A., Galle R.F.
M., Henderson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1013;
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Q9VHR2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Q9VHR2;
01-MAY-2000 (TrEM
01-MAR-2001 (TrEM
01-MAR-2001 (TrEM
CG11729 PROTEIN
CG11729
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                              Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                              287
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                                                                                                                                                                                                                                                                                                                                                                              1 GSLGGS
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bertins M.B., Balley D., Bhandari D., Britis P.
                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0038016; CG10042.
InterPro; IPR001739; MBD.
InterPro; IPR001065. ....
                                                                                                                                                                                                                    DNA-binding;
SEQUENCE 1
                                                                                                                                                                                                                                           PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE: PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001965;
InterPro; IPR002999;
InterPro; IPR000822;
                                                                                                                                                                                                                                                                 m; PF01429; MBD; 1.
pF00628; PHD; 1.
m; PF00096; zf-C2H2; 1.
RT; SM00391; MBD; 1.
RT; SM00391; PHD; 1.
RT; SM00333; TUDOR; 2.
RT; SM00355; ZnF_C2H2; 1.
                                                                                                          GSLGGS
                                                                                                                                                          Similarity 6; Conserv
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                       (TrEMBLrel. 13,
                                                                                                                                                          Conservative
(TrEMBLrel.
                                               PRELIMINARY;
                                                                                                                                                                                                                    Metal-binding; Zinc-finger.
081 AA; 119852 MW; D3417492763DD50B CRC64;
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Y.-H.C., Blazej
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Last sequence update)
Last annotation update)
                       Created)
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                                                                                                                                                         Score 30; DB 5; 1
Pred. No. 8.2e+02;
; Mismatches 0;
                                               PRT;
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RA Baeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Neison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Pari V., Reese M.G.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Dang S., Pan S., Pallard J., Pari V., Reese M.G.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhong C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhong C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhong C., Zheng L.,
RA Zheng X.H., Zhong F.N., Robin M., Zhong G., Zhong C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng R., Ra Firlm R., Shang R., Shang G., Zhong C., Zhong C.,
RA Zheng R., Shang R., Sha
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Best Local s
Matches (
Leishmania major.
Eukaryota; Euglenozoa; K
NCBI_TaxID=5664;
[1]
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01-AUG-1998
01-JUN-2001
STPK1.
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Pterygota; Neoptera;
Ephydroidea; Drosoph
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nes 6; Conserv
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1340 AA; 147657 M
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
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Pred. No. 1e+
0; Mismatches
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1e+03;
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Q62766;
                                 1347 GSLGGS 1352
                                                                                                                                                                                       "Isolation and characterization of a novel 322, which is transcriptionally suppressed
                                                                                                                                                                                                                                    STRAIN=FISHER; TISSUE=EMBRYO; MEDLINE=95257957; PubMed=7739556;
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; ABOULTY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; ABOULTY4; AACL4682.1; .
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000290; Ser_thr_kin_actsite.
Pfam; PF00069; pkinase; 4.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1557 AA; 167982 MW; 8C6955618BBD086A CRC64;
                                                                                                                                   SEQUENCE
                                                                                                                                              and ras.",

MO1. Cell. Biol. 15:2754-2762(1995).

EMBL; U23146; AAA79517.1; -.

InterPro; IPRO01573; PkinA_anch.
                                                                                                                                                                                                                 Gelman I.H.;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                          SSECKS
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Submitted (MAY-1998) to t
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STRAIN-FRIEDLIN;

Myler P.J., Audleman L., Hixson G., Kiser P., Lemley C., Ri
Sisk E., Sunkin S., Swartzell S., Westlake T., Magness C.,
Fu G., Ivens A., Stuart K.;
                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GSLGGS
                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 6; Conserv
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27
                                                     1 GSLGGS 6
                                                                           Similarity
6; Conserv
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                                                                             Conservative
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                                                                                                                                   AA:
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172498 MW;
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Last sequence update)
Last annotation update)
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Pred. No. 1.2
0; Mismatches
                                                                         Score 30; DB 11;
Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                           В.,
                                                                                                                                   CF78F2D161D9C7E2 CRC64
                                                                                                                                                                                                                          Tombler
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Chapline C., Mousseau B., Ramsay K

"Identification of a major protein

substrate in rat embryo fibroblast:

transformed cells.";

J. Biol. Chem. 0:0-0(1995).

EMBL; U41453; AADD378B.1;

InterPro; IPR001573; PkinA_anch.

SEQUENCE 1596 AA; 172411 MM; E
                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR00051; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GPA5;
Q9GPA5;
Q1-MAR-2001
Q1-MAR-2001
Q1-JUN-2001
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PKC BINDING PROTEIN AND SUBSTRATE.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rati
MCBI_TaxID-10116;
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Q9Z1F7;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-20Q1
                                                                                                                                  Pfam; PF
PRINTS;
PRINTS;
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                                    SMART;
SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                      Notch (AmphiNotch): evolutionary conservation of multiple domains in amphioxus and vertebrates."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases EMBL; Y12539; CAC19873.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-WHOLE LARVAE;
Holland L.Z., Burgtorf C., Holland N.D., Lehr
Holland L.Z., Burgtorf C., Holland N.D., Lehr
Abi-Rached L., Pontarotti P., Lardelli M.;
"Cloning and developmental expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Branchiostoma.
NCBI_TaxID=7739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Branchiostoma floridae (Florida lancelet) (Amphioxus)
Eukaryota: Metazoa; Chordata; Cephalochordata; Branch
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01-MAR-2001 (TrEMBLrel. 16, Last
01-JUN-2001 (TrEMBLrel. 17, Last
PUTATIVE NOTCH RECEPTOR PROTEIN.
                     SMART;
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Local
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                                                                                                         pe00023; ank; 6.
; pe00008; ege; 36.
; pe00066; notch; 3.
;ps pe00010; egebLood;
rs; pe00011; egeLAMININ.
rs; pe01452; NOTCH.
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               SM0024B; ANK; 6.; SM001B1; EGE_C3; 34.; SM00101; EGE_Ike; 13.; SM00001; EGE_Ike; 13.; SM00004; NL; 3.
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6; Conserv
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major protein kinase C binding
yo fibroblasts: Decreased expr
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Q9C6G9;
Q1-JUN-2001 (
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Q1-JUN-2001
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PROSITE;
PROSITE;
EGF-like
SEQUENCE
                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Ber Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-21173698; PubMed-11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLAGELLAR HOOK-BASAL CC0955.
SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=69394;
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5; Conserv
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PS50297; ANK_REP_REGION; 1.
PS00010; ASX_HYDROXYL; 1.
domain; Glycoprotein; Hydroxylation; Receptor.
2524 AA; 270969 MW; C2CA57E306D23EC9 CRC64;
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103 AA;
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(TTEMBLrel. 17, Last sequence update)
(TTEMBLrel. 17, Last annotation update)
OOK-BASAL BODY COMPLEX PROTEIN FLIE.
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(TrEMBLrel. 17, Last sequence update)
(TREMBLrel. 17, Last annotation update)
TRANSPOSASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.4e
1; Mismatches
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1.4e+02;
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                                                                          eudicots;
                                                                                         Tracheophyta;
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ock J.R.,
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B.,
RA Lingin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,
RA Milischer J., Miranda M., Nguyen M., Nierman M.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Best Local S
Matches 5
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Best Loc
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submitted (MAR-2000) to the
EMBL; AL162873; CAB85515.1;
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Bevan M., Peters S.A.,
Bancroft I., Mewes H.W
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01-OCT-2000 (
01-OCT-2000 (
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                              Q9HLK2
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 252 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000)
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L 28.4 KDA PROTEIN.
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Pred. No. 3.9e+02;
1; Mismatches 0;
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T 01-NOV-1996 (TrEMBLrel. 07
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TCD 5564 GENES STRB AND 6
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Best Local Similarity
Matches 5; Conserv
         Q9FL20;
Q9FL20;
Q9FL20;
Q1-MAR-2001
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Q1-MAR-2001
SIMILARITY TO
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SEQUENCE FROM N.A.
STRAIN-DSM 1728;
STRAIN-DSM 1728;
MEDLING-20479972; PubMed-11029001;
MEDLING-20479972; PubMed-11029001;
MEDLING-CONTROLOGY
MEDL
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Submitted (APR-1994) to the I
EMBL; X78972; CAA55568.1: -.
NON_TER 267 267
SEQUENCE 267 AA; 29777 MW.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
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NCBI_TaxID=33897;
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Nature 407.508-513(2000).
EMBL; AL445063; CAC11371.1;
Hypothetical protein; Complete
SEQUENCE 254 AA; 28322 MW;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
HYPOTHETICAL PROTEIN TA0226.
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Thermoplasma acidophilum
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(TrEMBLrel. 16, Created)
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TO MUTATOR-LIKE TRANSPOSASE.
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     RX. MEDLINE-20196006; PubMed-10731132;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burdon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Baldwin R.C., Busch R.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bartis J.F., Agbayani A., Buck J., Brokstein P., Brottler P.,
RA Burtls K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShon D.L.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson D.L.,
RA Nelson D.R., Pacleb J.M.,
RA Nelson D.R., Patltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Best L
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Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana features of the regions of 1.381,565 bp cover physically assigned Pland TAC clones."; DNA Res. 5:131-145(1998).
EMBL; AB010699; BAB10892.1; -.
SEQUENCE 280 AA; 31489 MW; 852051E61D0D1;
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STRAIN-COLUMBIA;
MEDLINE-98344145;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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Eukaryota; Metazoa; Arthropoda; Tra
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01-MAY-2000
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Tabata S.;
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ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 10;
Pred. No. 4.4e+02;
1; Mismatches 0;
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RA Adams M.D., Celniker S.E., Riothards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burdon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barler B.D., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krenison J.A., Ketchum K.A.,
RA Melson D.R., Nelson K.A., Nurnhy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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01-NOV-1998
01-JUN-2001
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; AE003757, AAP56600.i;
-Flybase; FBgn0039434; CG5468.
SEQUENCE 288 AA; 28669 MW; AC28B3BD48F180E6 CRC64;
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Eukaryota;
Pterygota;
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077475;
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5; Conserv
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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GTTEMBLTel.
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RESULT
OPENICATION
RC STRAIN-BERKELEY;

RX MEDLINE-20196006: PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Horli J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Dietz S.M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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MEDLINE-99208659; PubMed-10191082;

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Genomics 57:43-56(1999).

EMBL; AB010264; BAA32692.1; -.

EMBL; AB010264; BAA32689.1; -.

FlyBase; FBgn0025335; CG4585.

InterPro; IPR000462; CDP-OH_P_transf.
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ALIU X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
AL Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
AL Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
AL Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
AL Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
AL Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
AL Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
AL Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
AL Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
AL Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AL Wang Z.-Y., Wang A.H., Wang X.,
AL Wang Z.-Y., Wang A
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
MEDLINE-95239761; PubMed-7723040;
Beekwilder M.J., Nieuwenhuizen R.,
"Secondary structure model for the
"Secondary of beta.";
                                                                                                                                                                   Beekwilder M.J., Nieuwenhulzen R., van Duin J. Submitted (APR-1998) to the EMBL/GenBank/DDBJ EMBL; AF059242; AAC14698.1; -. 3978CB9E7E9D094
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=96190948; PubMed=8609616;

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Nol. Biol. 256:8-19(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteriophage MX1.
Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae; serogroup III.
NCBI_TaxID-75723;
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01-AUG-1998 (TrEMBLrel.
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RA Addams M.D. Celniker S.E., Lil P.W. Hoskins R.A. Golle R.F.,
RA Addams M.D. Celniker S.E., Lil P.W. Hoskins R.A. Golle R.F.,
RA Mannstides P.G., Scherer S.E., Lil P.W. Hoskins R.A. Golle R.F.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Hederson S.N.,
RA Bulcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bulcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bulcon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peilfer B.D.,
RA Mon K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beason K.Y., Benos P.V., Berman B.P., Bhanddri D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhanddri D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke G., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke G., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart M.K., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jelai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Helson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reihert K., Remigton K., Sanders R.D.C., Scheeler F., Shen H.,
RA Spler E., Spradiling A.C., Stapleton M., Stepse R., Wang A.H., Wan
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NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                        PRINTS; PR00027; PAIREDBOX. SMART; SM00351; PAX; 1.
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MEDLINE-20196006; PubMed-10731132;
Colorker S.E., Holt R.A.,
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SEQUENCE
                                                  PROSITE; PS00034; PAIRED_BOX; 1.
DNA-binding; Developmental protein; Nuclear protein; Paired
                                                                                                                                                                                               Pfam: PF00292;
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pfam; pr00292; pax; 1.
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Q1-NOV-1996
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                                                                                                                                                                                                                                                                                                              "Complex expression of keratins in goldfish optic nerve.";
J. Comp. Neurol. 340:269-280(1994).
EMBL; L09743; AAC368.1; -.
InterPro; IPR001564; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-OPTIC NERVE;
MEDLINE-94259853; PubMed-7515399;
Druger R.K., Fuchs C., Levine E.M., Park C.Y., Matthews J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schechter N.
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Sequence 12, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 16, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29,
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ALIGNMENTS

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Query Match
Best Local Similarity
Exches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                       ; INDIVIDUAL ISOLATE: Ig kappa peptide linker US-08-828-712-11
                                                                                                                                                      us-09-063-276-11
                                                                                                                       Sequence 11, Application US/09063276 Patent No. 6140113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                           GENERAL INFORMATION:
APPLICANT: Schneck, CAPPLICANT: O'Herrin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)508-910
TELEFAX: (202)508-9299
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
               TITLE OF INVENTION: MO
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 2
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schneck, Jonathan P. APPLICANT: O'Herrin, Sean
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/828,712 FILING DATE: 28-MAR-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                               1 GSLGGS 6
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                                                                                                                                                                                                                  GSLGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Banner & Witcoff, Ltd.
1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                              Conservative
                                                                                           Schneck, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
Banner & Witcoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202)508-9100
                                                                                                                                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                            Molecular Complexes Which Modify Immune Responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble Divalent and Multivalent Heterodimeric Analogs of Proteins
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Pred. No. 1.6e+05;
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                                                                                                                                                                                                                                                                                                            Length 6;
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   FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GSLGGS 6
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Query Match
Best Local Similarity
Matches 6; Conserv
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FILING DATE: 21-APR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/828/71
APPLICATION UMBER: 60/014/36
FILING DATE: 28-MAR-1996
APPLICATION UMBER: 60/014/36
FILING DATE: 28-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KASAN, SATAN A
REGISTRATION NUMBER: 32141
REGISTRATION NUMBER: 32141
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,
FILING DATE: 19-APRIL-1996
                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gelman, Irwin H.
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1001 G S
CITY: Washington
                                                                                                                                   COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Brumbaugh, Graves, STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                           10112-0228
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                                                                                   US/08/635,121
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Pred. No. 1.6e+05;
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US-08-014-153D-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/08014153D
GENERAL INFORMATION:
APPLICANT: Hadlock, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                TELEFAX: (415) 368-0709
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION UNMER: US/08/014,153D
FILING DATE: 05-Peb-1993
CLASSIFICATION : <Unknown>
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: US 07/653,091
FILING DATE: 08-FEB-1991
APPLICATION NUMBER: US 07/366,313
FILING DATE: 13-JUN-1989
APPLICATION NUMBER: US 06/948,270
FILING DATE: 13-DEC-1986
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A.
REGISTRATION NUMBER: G5.373
BFFFFRENCE/PACKET NIMMER: G4C1D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
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LENGTH: 1346 amino acids
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TELEFAX: 212-765-2519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: A3
                                                                   REFERENCE/DOCKET NUMBER: G4C1P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 369-9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method and Assay for HTLV NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Redwood City
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 5.3e+02;
""smatches 0;
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: E
US-09-041-991A-8
                                                        RESULT 6
US-09-041-991A-10
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                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MA.7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acids
TYPE: amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-041-991A-8
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   Sequence 10, Application US/09041991A
Patent No. 6107278
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                          Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6107278
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/N
SOFTWARE: PATENTIN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 13-MAR-198
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                 1 GSLGGS 6
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| 349 GSIGGS 354
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Toxins Active Against Pests NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sanders, Jay M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSLGGS
||:|||
10 GSMGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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2421 N.W. 41st Street, Suite A-1
Schnepf, H. Ernest
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narva, Kenneth
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                                                                                                                                                                                      93.3%;
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83.3%;
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Pred. No. 5.
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5.7e+02;
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Best Local Similarity
""" best 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                     US-08-704-931-6
; Sequence 6, Application US/08704931
; Patent No. 5885797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
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CORRESPONDENCE ADDRESS:
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APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Sanders, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

v APPLICATION NUMBER: US/08/704,931 FILING DATE:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 5885797el DNA Sequences Encoding Proteins TITLE OF INVENTION: Involved in Myogenesis NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                               APPLICANT: Chen, Chao-Min
APPLICANT: Kraut, No. 5881
APPLICANT: Groudine, Mark
APPLICANT: Weintraub, Harr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Florida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 GSIGGS 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                            COUNTRY: USA
ZIP: 98101
                                                                                                                                                                            STATE: WA
                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSLGGS 6
                                                                                                                                                                                             Seattle
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Pred. No. 5.7e+02;
"'mmatches 0;
                                                                                                                                                                                                                 , PLLC
Suite 1313
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-931-2
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; Sequence 2, Application US/08704931
; Patent No. 5885797
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COMPUTER: IBM PC COMPATIBLE
SOPTWARE: PATENTIN ROLDS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704.931
FILING DATE:
CLASSTETT:
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Best Local Similarity
Matches 5; Conser
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-683-1496
TELEFAX: 206-682-0446
INFORMATION FOR SEQ. ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Chen,
                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: King, Jeffrey J
REGISTRATION NUMBER: 38.515
REGISTRATION NUMBER: HUll
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-683-1496
                                                                                                                   TELEFAX: 206-682-0446 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TYPE: amino acids
TOPOLOGY: line
WOLECHE
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NAME: King, Jeffrey J
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5885797el DNA Sequences Encoding Proteins TITLE OF INVENTION: Involved in Myogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kraut, No. 588
APPLICANT: Groudine, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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STREET: 12-1
STREET: 12-1
STREET: 12-1
STREET: 12-1
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1218 Third Avenue, Suite 1313
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Pred. No. 2.1e+02;
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Query Match
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Matches 5; Conserv

Conservative

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Score 27; DB 2; pred. No. 3.3e+02; 1; Mismatches (

DB 2;

Length 246;

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US-09-237-543-4
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GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 206-683-1496
TELEFAX: 206-682-0446
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No.
                                                                                                                                                                          Sequence 4, Application US/09237543A Patent No. 6143540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: King, Jeffrey J
REGISTRATION NUMBER: 38,515
REFERENCE/DOCKET NUMBER: HU11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-683-1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Chao-Min (Amy)
APPLICANT: Kraut, No. 5885797bert
APPLICANT: Groudine, Mark
APPLICANT: Weintraub, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             120 GALGGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 5885797el DNA Sequences Encoding Proteins
TITLE OF INVENTION: Involved in Myogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1218 T
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/704,931 FILING DATE:
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1218 Third Avenue, Suite 1313
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                                                                                                                                                                                                                                                                                                                                                              Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 12 US-09-237-543-2

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; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-633-148-4
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Best Local Similarity
Yorkches 5; Conserva
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; OTHER INFORMATION: protein kinase domain
US-09-237-543-4
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                                                            Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                     TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
309 GSVGGS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                            TYPE: amino acid
                               1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                Conservative
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                                                                                                                                                             peptide
                                                                            90.0%;
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83.3%;
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                                                            Pred. No. 4.3e
1; Mismatches
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Pred. No. 3.4e+02;
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                                                                                           Length 318;
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                                                            Indels
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-237-543-2
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Best Local S
Matches 5
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APPLICANT: Kapeller, Rosana
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION UNMEER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application Patent No. 5864018
Nest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SIZEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
APPLOBLEM ACCEMENT INCOMMENTION:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MORSER, MICHAEL J. APPLICANT: NAGASHIMA, MARIKO APPLICANT: HOLLANDER, DORIS A
                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 GSLGGA 85
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les 5; Conservative
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                                                                                                                     TOPOLOGY:
                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                         amino acid
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                                                                                                                                                                              340 amino acids
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                                                                                                                     linear
                                                                                                peptide
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    90.0%;
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Pred. No. 4.4e+02;
    Score 27; pred. No.
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      DB 2;
4.6e+02;
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                    Length 340;
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Best Local Similarity
The 5; Conserve
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US-09-375-419-6
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Patent No. 6060054
GENERAL INFORMATION:
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                                                                                                                                                                                Sequence 6, Application US/09375419 Patent No. 6264950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (303) 863-9223
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEDIIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: CONNell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 28
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
                                                                                                                  APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOV
TITLE OF INVENTION: LYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 GSVGGS 336
                                                                                       CORRESPONDENCE ADDRESS
                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            156 GSLGGT 161
                 STREET: 1700 Lincoln Street, 35th Floor CITY: Denver STATE: Colorado COUNTPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Colorado
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              COUNTRY:
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1700 Lincoln Street, 35th Floor
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            U.S.
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                                                                                                                                       NOVEL PRODUCT AND PROCESS FOR T
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Pred. No. 4.7e+02;
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COMPUTER READABLE FORM:

TYPE: Floppy disk

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US-08-464-266-2
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NAME: CONNELL, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE, DOCKET NUMBER: 2879
TELECHONE: (303) 863-9700
TELEPAX: (303) 863-9223
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08464266 Patent No. 5641652
                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/013,975
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/497,935
FILING DATE: 22-FEB-1990
ATTORNEY/ACENT INFORMATION:
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                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,266
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ORO, Ph.D., ANTHONY E.
APPLICANT: EVANS, Ph.D., RONALD M.
TITLE OF INVENTION: INSECT RETINOID-LIKE RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                     NAME: Reiter,, Stephen E. REGISTRATION NUMBER: 31,1
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 444 South
CITY: Los Angeles
REFERENCE/DOCKET NUMBER: P41 9966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/375,419
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                                                                                                                                                                                                                                                                                                                                                                                             CA
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444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 amino acids
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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4.7e+02;
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US-08-464-272-2
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Best Local Similarity
Matches 5; Conserva
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Query Match
Best Local
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                                                                                                                     INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    FILING LALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/013,975
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                      MOLECULE TYPE:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ORO, Ph.D., ANTHONY E. APPLICANT: EVANS, Ph.D., RONALD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
                                                                                                  TYPE: a
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                                                                                   TOPOLOGY:
                                                                                                                                                                                            REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
                                                                                                                                                                                                            NAME: Reiter,, Stephen E. REGISTRATION NUMBER: 31,1
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                               amino acid
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                                                                                                            513 amino acids
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90.0%;
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Flower Street, Suite 2000
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Score 27; DB 1;
Pred. No. 7.1e+02;
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Pred. No.
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           Length 513;
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Best Local Similarity
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                                                                                                        Sequence 2, Application US/08486403 Patent No. 6281330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08464514
Patent No. 6265173
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 546-939
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE TITLE OF INVENTION: STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SEGRA
                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MCKEOWN, MICHAEL B.
                                                                                                                                                                                                       200 GSVGGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Reiter,, Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/464,514 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 444 South
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                     1 GSLGGS 6
                                                                            INFORMATION:
CANT: EVANS, RONALD M.
                                                                                                                                                                                                                                                                                                                                                                                          amino acid
   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                          513 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORO, ANTHONY E
              SEGRAVES, WILLIAM A. YAO, TSO-PANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619)
                                                          MCKEOWN, MICHAEL B.
                                                                                                                                                                                                                                                                    Conservative
                                               ORO, ANTHONY E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVANS, RONALD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRETTY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        ) 546-9392
TO NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSO-PANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546-4737
                                                                                                                                                                                                                                                                                   90.0%;
 MULTIMERIC FORMS OF MEMBERS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHROEDER, BRUEGGEMANN & CLARK
Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WILLIAM A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07/907,908
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                 DB 4;
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Query Match
Best Local Similarity
"---hes 5; Conserva
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                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08642406A Patent No. 5959177
GENERAL INFORMATION:
APPLICANT: Hein, Mich B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E
REGISTRATION UNMBER: 31192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 546-93
INFORMÁTION FOR SEQ ID NO:
          COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,406A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 02-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ST.
TITLE OF INVENTION: UL:
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                               STREET: LOUG
CITY: LA Jolla
CMATE: California
                                                                                                                                                                                                                                                                        APPLICANT: Hiatt, Andrew C. APPLICANT: Ma, Julian K.C. TITLE OF INVENTION: TRANSGENIC TITLE OF INVENTION: SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 444 South
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                       ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE STREET: 10666 No. 5959177th Torrey Pines
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                                                                                                                                      92037
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(619) 546-9392
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03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE ULTRASPIRACLE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%;
                                                                                                                                                                                                                                                                            TRANSGENIC PLANTS EXPRESSING ASSEMBLED SECRETORY ANTIBODIES
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US 07/591,823

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RESULT 21
US-08-434-000A-2
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TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 554-2937
TELECHAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08434000A Patent No. 6046037
                           CLASSIFICATION: 435
PRIOR APPLICATION DATA: including app
PRIOR APPLICATION DATA: described bel
PRIOR APPLICATION DATA: described bel
APPLICATION NUMBER: 08/367,395
FILLING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34/613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOSLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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FILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APRIL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 02-0CT-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 GNLGGS 255
                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 624 amino acids
TYPE: amino acid
TOPOLOGY: linear
TELEFAX: (619) 552-8400
TELEFAX: (619) 552-0159
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nes 5; Conserv
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REGISTRATION NUMBER: 33,950
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California
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633 West Fifth Street
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                                                                                                                                                : including application
: described below:
08/367,395
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Pred. No. 8.7e+02;
                                                                                                                                                                                                                                                                                                                     DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                             1.44 Mb
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-312-157-2
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US-09-312-157-2
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Best Local Similarity bo...
Thes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: 773 amino acids
                                                                                                             SEQUENCE LISTING SEQUENCE CHARACTERISTICS:
                                                                                                                                                             NAME: Guise, Jeffrey W. REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEY: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 GNLGGS 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSLGGS 6
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-199
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/434,000 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION:
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                           DESCRIPTION:
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Pred. No. 1.1e+03;
1; Mismatches 0
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                                                                                                                                                                                                                                                            34,613
              Rabbit polyimmunoglobulin receptor
D: 2:
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Query Match Best Local Similarity

90.0%;

Score 27; DB 4; Length 773; Pred. No. 1.1e+03;

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                                                                                                                     Sequence 13, Application US/08867941 Patent No. 5977337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 2993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                       GENERAL INFORMATION:
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                                 APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, MICHAI H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STRAND, KURT
APPLICANT: TODARO, GEORGE J.
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                                                                                                                                                                                                                             133 GSLGGN 138
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STATE: Californ
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TELEX: 70614:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/680,326
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                                                                     Du, Run-Pan
                                                                                     Loosmore, Sheena M
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                                                                                                                                                                                                                                                                                                                                                                                             linear
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Pred. No. 1.4e+03;
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Query Match
Best Local Similarity
Services 5; Conserve
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-UNU-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELECOMMUNICATION INFORMATION:
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SOFFWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
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CORRESPONDENCE ADDRESS:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel |
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OTTY: Toronto
Ontario
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ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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ZIP: M5G 1R7
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                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                   STATE: Ontario
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M5G 1R7
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                                                                                                                                                                                                                                                                      330 University Avenue
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Pred. No. 1.4e+03;
                                                                                                            Version #1.30
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                                                                                   Query Match
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Patent No. 6
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                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24 973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,658 FILING DATE: 08-MAX-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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APPLICANT: Klein, Michel H
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                                                                                                                                         TYPE: amino a STRANDEDNESS: TOPOLOGY: lin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
175 GALGGS 180
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                                                      Local Similarity
nes 5; Conserv
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STRANDEDNESS: sir
TOPOLOGY: linear
                             1 GSLGGS 6
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M5G 1R7
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                                                                                                                                                                   amino acids
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6th Floor, 330 University Avenue
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                                                      Conservative
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Quijun Wang
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                                                Score 27; DB 4; Le
Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
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US-09-074-658-17
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                 Sequence 12, Appli
Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserva
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ANAMER: STEWART MEDICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                   GENERAL INFORMATION:
APPLICANT: LOSSMOTE, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
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                                                                    CORRESPONDENCE ADDRESS
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LENGTH: 985 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
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           STREET: 6th F1
CITY: Toronto
                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'RY: Canada
M5G 1R7
Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ontario
                                                                                                                                                                                                                                                  Application US/08867941
                                  6th Floor,
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Quijun Wang
Yang, Yan-Ping
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                          Sim & McBurney
h Floor, 330 University Avenue
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h Floor, 330 University Avenue
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Pred. No. 1.4e+03;
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                            ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 59//22.
Patent No. 59//22.
TONTRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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APPLICANT:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
                  SEC ENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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190 GALGGS 195
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STRANDEDNESS: sir
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o. 5977337
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M5G 1R7
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R READABLE FORM:
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5; Conserv
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6th Floor, 330 University Avenue
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1000 amino acids
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Pred. No. 1.4e+03;
1; Mismatches 0;
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RESULT 30
US-09-074-658-12
; Sequence 12, Applic
; Sequence 10, 6184371
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-16
RESULT 31
US-09-074-658-16
; Sequence 16, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6th FlucITY: Toronto STATE: Ontario
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                                                                                                        190 GALGGS 195
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael | REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Klein, Michel
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Pred. No. 1.4e+03;
                                                                                                                                                                    Score 27; DB 4;
Pred. No. 1.4e+03;
1; Mismatches 0
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                                                                                                                                                                                              DB 4; Length 1000;
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Loosmore,

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08484438 Patent No. 5811098 Patent No. 5811098 5780031
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                    NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                 APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                        APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GALGGS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 78
                                      COUNTRY: U.S.A. ZIP: 10036-2711
                                                                       CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6th ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ontario
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                                                     New York
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6th Floor, 330 University Avenue
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-438-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-074-658-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Appl. Patent No. 618437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA:

APPLICATION UNBER: US/09/074,658 FILING DATE: 08-MAY-1998 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1060 GNLGGS 1065
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yang, Yan-Pin
APPLICANT: Klein, Michel
TITLE OF INVENTION: LACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: 14-OCT-1994
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                                                                                                                                                                                                                                               STREET: 6th Floc
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    COUNTRY:
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nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/150,704 FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/484,438 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                      'RY: Canada
M5G 1R7
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                                                                                                                                                                                                                                                                               E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09074658
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Quijun Wang
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Pred. No. 1.9e+03;
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US-09-074-658-11
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Best Local S
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Best Local :
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                                                                                                                                                                                                                                         TELEFAX: (416) 595-110 INFORMATION FOR SEQ ID NO:
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1668 GALGGS 1093
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
OUR PROTECT NUMBER: COMPANY CES
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2439 amino acids
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel
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APPLICANT: Run-Pan Du
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Toronto
STATE: Ontario
                                                               Local Similarity hes 5; Conserv
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STRANDEDNESS: single
                                                                                                                                                            TOPOLOGY: 11r
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                                                                                                                                                                                              TYPE:
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                                 1 GSLGGS 6
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M5G 1R7
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) 595-1163
-- NO: 11:
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                                                             Score 27; DB 4; LC. Pred. No. 3.6e+03; Pred. No. 3.6e+03;
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Pred. No. 3.6e+03;
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                                                                                             Length 2439;
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
Type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-609-716-16
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Best Local Similarity
~~+~hes 5; Conserve
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US-07-609-716-67
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                                                                                                                                                                   Sequence 67, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
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Patent No. 5514581
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly |
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETLYAM I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/609,716
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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                                                                              CITY:
STATE:
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4 GSFGGS 9
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ZIP: 94111
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CITY: San Francisco
                                                        COUNTRY:
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                                                                            San Francisco
: CA
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Pred. No.
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27;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                           APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
               APPLICATION NUMBER: 1
FILING DATE: 29-OCT-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993
                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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TOPOLOGY: lin
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SYSTEM: PC-DOS/MS-DOS
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UMBER: US 06/927,258
04-NOV-1986
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83.3%;
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Pred. No.
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Query Match
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                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/ACENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/482,085B FILING DATE: 07-JUN-1995
                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
   REFERENCE/DOCKET NUMBER:
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                           Trecartin, Richard F.
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Crissman, John W
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Pollock, Thomas J.
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Chambers, James
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A-55186-6/RFT/MTK
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Pred. No.
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989

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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
FILING DATE: 06-NOV-1990
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Best Local S
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APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.
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INFORMATION FOR SEQ ID NO:
                                                                                  TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
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LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
PERANDEDNESS: single
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                                                                                                                   REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
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APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
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Local Similarity 83.3%;
hes 5; Conservative
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US-08-475-411A-67
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                                                                                         ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-475-411A-67
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 07/269,429

PRIVING DATE: 09-NOV-1988

PRIOR APPLICATION NUMBER: US 07/214,618

PRIOR APPLICATION NUMBER: US 07/114,618

PRIOR APPLICATION NUMBER: US 06/927,258

PRIOR APPLICATION NUMBER: US 06/927,258

APPLICATION NUMBER: US 06/927,258

PRIOR APPLICATION NUMBER: US 06/927,258

APPLICATION NUMBER: US 06/927,258

PRIVING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK

TELEPHONE: 415-781-1989

TELEPHONE: 415-781-1989
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 Matches
                 Query Match
Best Local
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/609,716
APPLICATION UMBER: US 07/609,716
FILING DATE: 06-NOV-1990
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APPLICANT: Ferrari, Franco APPLICANT: Cappello, Joseph
                                                                                                                                                                                                                         TELEPHONE: 415-781-19
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DE PC -DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Functional Recombinantly Prepared TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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Similarity
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amino acid
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   Conservative
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83.3%;
                 86.7%;
Score 26; DB 4; pred. No. 27; 0; Mismatches
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5: /cgn2_6/ptodata/2

6: /cgn2_6/ptodata/2
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Maximum
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US-08-461-990B-26
US-08-451-990B-26
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11, Appli
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US-08-485-963A-50
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S252466-6
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US-08-984-618-125-12
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US-08-624-125-2
US-08-624-125-2
US-08-634-514-2
US-08-634-514-2
US-08-634-514-2
US-08-644-272-2
US-08-644-272-2
US-08-655-792E-9
US-08-664-318E-4
US-09-938-31-25
US-08-938-291A-6
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US-08-938-291A-6
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US-08-938-291A-6
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US-08-648-322-10
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US-08-648-322-10
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sequence
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ALIGNMENTS

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; Sequence 10, Application US/08828712
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NAME: KBGNT, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,508-9,100
                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: p
HYPOTHETICAL: NO
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                              APPLICANT: Schneck, Jonathan
APPLICANT: O'Herrin, Sean
TITLE OF INVENTION: Molecular Complexes Which
TITLE OF INVENTION: Modify Immune Responses
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0: FILING DATE: 28-MAR-1997 CLASSIFICATION: 514
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CITY: Washington
STATE: D.C.
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Banner & Witcoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100 TELEFAX: 202-508-9299
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/828,712
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: 60/014,367
FILING DATE: 28-MAR-1996
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MEDIUM TYPE: Diskett
           APPLICATION NUMBER: US/08/974,546 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                          SOFTWARE: FastSEQ for V
                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Je
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                              APPLICANT:
                                              COMPUTER: IBM COMPTON OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
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REGISTRATION NUMBER: 3214
REFERENCE/DOCKET NUMBER:
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SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER:
                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                       STATE:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 21-APR-1998
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3174 Porter Dr.
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100.0%; Pred. No.
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2071
TYPE: PRT
ORGANISM: Ashbya gossypli
US-09-415-522-6
                                                                                                                  US-08-461-990B-14
; Sequence 14, Application US/08461990B
; Patent No. 5851810
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Best Local Similarity
""" 6; Conserva
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US-09-415-522-6
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APPLICANT: Gaffney, Thomas
APPLICANT: Wendland, Juergen
APPLICANT: Wendland, Juergen
APPLICANT: Philippsen, Peter
TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
TITLE OF INVENTION: Development
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Best Local Similarity
Matches 6; Conserv
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Patent No. 6291660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/415,522A CURRENT FILING DATE: 1999-10-08 NUMBER OF SEQ ID NOS: 28
                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                          APPLICANT: JOHN S. BLANCHARD
TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        199 GGGTSG 204
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CLONE: 2525691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
STREET:
                                                                                                                                                                                                                                                        1 GGGTSG 6
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                ADDRESSEE:
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90 PARK AVENUE
                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0
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                AMSTER,
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               ROTHSTEIN & EBENSTEIN
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Pred. No. 9.1e+02;
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Pred. No. 1.9e+02;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    DB 4; Length 2071;
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Query Match
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                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOCTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,990B
FILING DATE: JUNE 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG J. ARNOLD
REGISTRATION NUMBER: 34,287
REFERENCE/DOCKET NUMBER: 96700/370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08461990B Patent No. 5851810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/461,990B
FILING DATE: JUNE 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG J. ARNOLD
REGISTRATION NUMBER: 34,287
REFERENCE/DOCKET NUMBER: 96700/370
TELECOMMUNICATION INFORMATION:
TELECHHOME: (212) 697-5995
TELECHHOME: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:

DESCRIPTION: PROTEIN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: B. STEAROTHERMOPHILUS
INDIVIDUAL ISOLATE: ALANINE DEHYDROGENASE
                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                        STREET: 90 PARI
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                              90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                               JOHN S. BLANCHARD
VENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
VENTION: PHENYLALANINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                AMSTER, ROTHSTEIN & EBENSTEIN
286-0854 or 286-0082
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    Mismatches

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Query Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                          APPLICATION NUMBER: US 08/258
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lam, Suerc...
APPLICANT: Hammer, Philip E.
ADDITICANT: van Pee, Karl-Heinz
Cabine
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
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DESCRIPTION: PROTEIN

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: B. STEAROTHERMOPHILUS

INDIVIDUAL ISOLATE: ALANINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ligon, James M. APPLICANT: Hill, Dwight S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/028,934 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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67 GGGTAG 72
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amino acid
GY: linear
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Pred. No. 1.7e+02;
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                              Query Match
Best Local S
Matches 5
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/ACENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CTELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                    TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/258,261B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes for the sy
TITLE OF INVENTION: antipathogenic s
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                        MOLECULE TYPE:
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CLASSIFICATION:
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                                             Local Similarity
                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10532
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                                                                                                                                                                       LENGTH:
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1 GGGTSG 6
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                                                                                                                                                                    538 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                              Conservative
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Beck, James Joseph
Hill, Dwight Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals, John Andrew
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                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephen Ting
er, Phillip E.
                                             90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas Deane
                                                                                                                                                                                                                                                                 CGC 1506/CIP3
                                           Score 30; DB 1;
Pred. No. 7.9e+02;

    Mismatches

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Pred. No. 7.9e+02;
                             Mismatches
                                                          Length 538;
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US-08-457-342-2
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                                                                   Sequence 2, Application Patent No. 5662898
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application Patent No. 564377
GENERAL INFORMAT
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM; PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION UMBER: US/08/456,837
FILING DATE: 01-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                       APPLICANT:
                                                      APPLICANT:
     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hammer, Phillip E.
APPLICANT: UKnes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Jos
APPLICANT: Hill, Dwight St-
APPLICANT: Ryals, John And
                                                                                                                                                                                    1 GGGTSG 6
||||:|
12 GGGTAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hawthorne
                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                         Similarity
5; Conserv
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                                                                                                     Application US/08457342
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Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
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Hill, Dwight Steven
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                             linear
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGC 1506/CIP3
                                                                                                                                                                                                                                                                      Score 30; DB 1;
Pred. No. 7.9e+02;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                      Length 538;
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RESULT 11
US-08-457-646A-2
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Patent No.
GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICATION NUMBER: US 08/457,20:
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GC 150
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: line

VOLECUIP
                                   APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                         12 GGGTAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                               1 GGGTSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                   2, Application US/08457646A
5. 5679560
                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                         Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
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                                                                                                                                        Gaffney, Thomas Deane
                                                                                                                                                          Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                               Schupp, Thomas
Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/457,205
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; Pred. NO. 7.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
7.9e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5698425
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/-
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258
FILING DATE: 08-JUN-1994
ATTORNEY_AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FO-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                ZIP: 10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                            ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGTSG 6
                                                                                                                                            Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08458076A
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Beck, James Joseph
Hill, Dwight Steven
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83.3%;
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Pred. No. 7.9e+02;
1; Mismatches 0;
     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 538;
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RESULT 13
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/ACENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GCC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                  COUNTRY: USA
ZIP: 10532
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                         APPLICATION NUMBER: US/08/457,335A
FILING DATE: 01-UUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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FILING DATE: ATTORNEY/AGENT
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12 GGGTAG 17
                                                                                                                                                                                                                                                                                                                            CITY: Hawthorne
STATE: NY
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Local Similarity 83.3%;
hes 5; Conservative
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                APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 amino acids
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Hammer, Phillip E.
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Pred. No. 7.9e+02;
1; Mismatches 0;
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US-08-729-214-2
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FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 2:
FEORIEST CHARACTERISTICS:
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-457-335A-2
Query Match
Best Local Similarity 83.3
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08729214
Patent No. 5817502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: 1
APPLICANT: 1
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGTSG 6
||||:|
12 GGGTAG 17
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Elmer, James : REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                  linear
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                                          90.98;
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                     Score 30; DB 2; Le
Pred. No. 7.9e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1;
Pred. No. 7.9e+02;
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                                                      Length 538;
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                     Indels
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                    0;
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                    Gaps
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                    0;
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US-09-028-934-2; Sequence 2, A
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US-08-729-214-24
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                                                                  GENERAL INFORMATION:
APPLICANT: Ligon, J
APPLICANT: Hill, Dw
APPLICANT: Lam, Ste
                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        Query Match 90.5
Best Local Similarity 83.3
Matches 5; Conservative
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                                    APPLICANT:
     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/729,214
FILLING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYDE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                              12 GGGTAG 17
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CITY: Tarrytown
STATE: NY
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                                                                                                                                          , Application US/09028934
6117670
Lam, Steven T.
Hammer, Philip E.
van Pee, Karl-Heinz
Kirner, Sabine
Young, Thomas R.
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                                                                                    Ligon, James M.
Hill, Dwight S.
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Pred. No. 7.9e+02;
1; Mismatches (
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Pyrrolnitrin Biosynthesis Genes and Uses

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US-09-028-934-24
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APPLICATION NUMBER: US 08/729,214
APPLICATION NUMBER: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Medigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                              TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Philip B.
COMPUTER READABLE FORM:
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC
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||||:|
12 GGGTAG 17
                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                COUNTRY:
                                                                                  STREET:
                                                                                                  ADDRESSEE:
                   27709
                                              Research Triangle Park
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                                                                                   3054 Cornwallis Road
                                                                                                                                                                                    van Pee, Karl-Heinz
Kirner, Sabine
Young, Thomas R.
                                 USA
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                                                                                                  No. 6117670artis Corporation
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Query Match
Best Local Similarity
Thes 5; Conserv
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SEQ ID NO 2
LENCTH: 543
TYPE: PRT
ORGANISM: Fusarium
US-09-199-229-2
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RESULT 19
US-09-443-087-2
; Sequence 2, Application US/09443087
                                                                                                                                      Query Match
Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yaver, Debbie S.
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Rey, Michael W.
APPLICANT: Rey, Michael W.
TITLE OF INVENTION: Polypeptides Having Choline Oxidase
TITLE OF INVENTION: Activity and Nucleic Acids Encoding
FILE REFERENCE: 5735.000-US
CURRENT APPLICATION NUMBER: US/09/199,229
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/729
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 538 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 919-541-8689
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                                                                                  APPLICATION NUMBER:
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Pred. No. 7.9e+02;
""ematches 0;
                                                                                                                                                       1; Mismatches
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Pred. No. 8e+02;
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US-08-955-848A-45
; Sequence 45, App
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; TYPE: PRT
; ORGANISM: Fusarium venenatum
US-09-443-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Polypeptides Having Choline Oxidase TITLE OF INVENTION: Activity And Nucleic Acids Encoding CURRENT APPLICATION NUMBER: US/09/443,087 CURRENT FILING DATE: 1999-11-18 EARLIER APPLICATION NUMBER: 09/199,229 EARLIER FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,848A
FILING DATE: 21-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,165
FILING DATE: 25-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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APPLICANT: Mc Wherter, Charles
APPLICANT: Feng, Yiqing
TITLE OF INVENTION: No. 5969105
TITLE OF INVENTION: Agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Debbie Yaver
APPLICANT: Randy M. Ber
APPLICANT: Michael W. R
                                                                                                                        REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C--
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 60680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: G. D. Searle & Co. STREET: P.O. Box 5110
TYPE: amino acid
STRANDEDNESS: sir
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nes 5; Conservative
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single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 5969105el Stem Cell Factor Receptor
                                                                     45:
                                                                                                                                                            C-2992/1
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Pred. No. 8e+02;
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RESULT 22
US-08-256-156A-2
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Best Local Similarity
Thes 5; Conserve
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US-08-501-253A-9
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                                Sequence 2, Application US/08256156A
Patent No. 5837821
GENERAL INFORMATION:
APPLICANT: Wu, Anna M.
TITLE OF INVENTION: No. 5837821e
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION UNMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Biotherapeutic Agents Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Uckun, Fatih
APPLICANT: Tumer, Nilgun
                                                                                                                                                                                                                                                  Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 11-JUL CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Minneapolis STATE: MM
                                                                                                                                                                                          7
                                                                                                                                                                                                                   1 GGGTSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08501253A
                                                                                                                                                                                                                                                                                                                                                                                    15 amino acids
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90 South 7th Street,
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                       linear
Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: US/08/501,253A
11-JUL-1995
                                                                                                                                                                                                                                                                87.9%;
83.3%;
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83.3%;
                                                5837821el Antibody Constructs
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Pred. No. 47;
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Pred. No. 47;
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RESULT 23
US-08-377-687-39
; Sequence 39, Application US/08377687
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APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION UMBER: 30,377
REFERENCE/DOCKET NUMBER: 2124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,156A
FILING DATE: 24-JUN-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 24 amino TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGTSG 6
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83.3%;
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Pred. No. 71;
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; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-377-687-39
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Best Local Similarity
Thickes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: BROEKA
                                                                                              TELEPHONE: 202-861-30
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION UMBER: US 08/
APPLICATION UMBER: US 08/
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,77
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
TYPE: amino acids
TYPE: amino acids
STRANDENESS: single
TOPOLOGY: lines-
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN STREET: 1100 NEW Y CITY: WASHINGTON STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BROEKAERT, WILLEM F.
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83.3%;
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                                                                                                                                               16,773
ER: 99042/SEE.36525/US/A
                                                                                                 39:
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Pred. No.
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MOLECULE TYPE: -777-192-39

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RESULT 26
PCT-US96-01720-10
; Sequence 10, Application PC/TUS9601720
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US-08-971-982-39
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Best Local Similarity
"Atches 5; Conserva
                                                                                                                                                       Matches
                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                   1 GGGTSG 6
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24 GGGSSG 29
                                                                                                                                                   Local Similarity es 5; Conser
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                                                                                                                                                                                                                                                MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/002,480 FILING DATE: 04-JAN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TERRAS, FRANKY R.G.
TATLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHAM DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                LENGTH: 42 amino acids
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                                                                                                                                                   Conservative
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83.3%;
                                                                                                                                            Score 29; DB 4; Lei
Pred. No. 1.2e+02;
"" matches 0;
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Pred. No. 1.2e+02;
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; TOPOLOGY: 1;; MOLECULE TYPE: PCT-US96-01720-11
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Best Local Similarity
""tohes 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application PC/TUS9601720 GENERAL INFORMATION:
                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,055
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
                                                                                              REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,055
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                STRANDEDNESS:
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                                                                                    LENGTH:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                amino acid
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                                   linear
                 protein
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83.3%;
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Pred. No. 1.9e
0; Mismatches
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1.9e+02;
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RESULT 29
US-08-481-658B-50
US-08-481-658B-50; Sequence 50, Application US/08481658B; Patent No. 5955075;
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US-08-325-253-10
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Best Local Similarity
"""hes 5; Conserv
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NUMBER OF SEQUENCES:
                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-April-1992
ATTORNEY/AGENT INFORMATION:
NAME: W. MUITAY SPEULIL
REGISTRATION NUMBER: 32,943
REFERENCE/NOTURE: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Hans Rink
APPLICANT: Markus Gr(tter
APPLICANT: John Peter Priestle
APPLICANT: John Peter Briestle
APPLICANT: Albert Schmitz
TITLE OF INVENTION: Peptide Derivatives Corresponding to
TITLE OF INVENTION: the Carboxy Terminal Sequence of Hirudin
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/00908
FILING DATE: 15-April-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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59 GGGTGG 64
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FILING DATE: 20-OCT-1994
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5, 5686564
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Research Triangle Park
: No. 5686564th Carolina
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Zavada, Jan
Pastorekova, Silvia
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83.3%;
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0; Mismatches 1;
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Pred. No. 2.
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US-08-481-658B-50
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US-08-477-504A-50
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Best Local Similarity
Matches 5; Conserv
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-435-203
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORREY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: U.STREET: Tiburon
CITY: Tiburon
California
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
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TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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MOLECULE TYPE:
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
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STREET: b ...
CTTY: Tiburon
Califor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                       COUNTRY:
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VENTION: MN Gene and Protein
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Pred. No. 2.5e+02
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US-08-486-756A-50
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Best Local :
                         TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                              NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
ADDITION WINDELSTON
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/486,756A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
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DESCRIPTION:
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              ENGTH:
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amino acid
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83.3%;
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Pred. No. 2.5e+02;
"'amatches 0; Indels
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US-08-485-862B-50
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Best Local Similarity
"~+~hes 5; Conserva
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; DESCRIPTION:
US-08-486-756A-50
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                                                          Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                        NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
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1 GGGTSG 6
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13 GGGSSG 18
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                                                                      Local
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                                                          Similarity 5; Conserv
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                                                          Conservative
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                                                                                                                                            Region of homology to collagen alpha l chain
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83.3%;
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                                                                      87.9%;
83.3%;
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                                                                     Score 29; DB 2;
Pred. No. 2.5e+02;
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Pred. No. 2.
                                                         Mismatches
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Best Local Similarity
                                                                                                                                                                                  Sequence 50, Application US/08485863A
Patent No. 6093548
                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
APPLICANT: MN Gene an
                                                                                APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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                                                                                                                                               APPLICANT: Zavada, Jan
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                                                                                                                                                                                                                                                                                    13 GGGSSG 18
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                 STREET: 6 Mar
CITY: Tiburon
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REGISTRATION NUMBER: 30,863
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STATE: California
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6 Mariposa Court
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6 Mariposa Court
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83.3%;
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Pred. No. 2.5e+02;
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Thes 5; Conserve
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/ACENT INFORMATION:
NAME: Lauder, Leona L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
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CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REGERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                STREET: 303 ... CITY: San Francisco
                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 APPLICATION NUMBER: US/08/485,049D FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: Region of DESCRIPTION: 1 chain
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                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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83.38;
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                                30,863
                   D-0021.3E
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Pred. No.
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Best Local Similarity
"-+ches 5; Conserve
US-08-905-223-319
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                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 319:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 319
Patent No. 6
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APPLICANT: Edwards, Jean-Bap
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 50.
STREET: San Diego
CITY: San Diego
CTATE: California
                                                                                            FEATURE:
                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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DESCRIPTION:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
     NAME/KEY: sig_peptide
LOCATION: -29...1
LDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: SCOIE 5.7
OTHER INFORMATION: seq SPAFLAVAGPGWA/RP
                                                                                                                                                                                                                                                                                                               NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: Win95
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                                                                                                           TISSUE TYPE:
                                                                                                                          ORGANISM:
                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                  AMINO ACID

GY: LINEAR
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GY: linear
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                                                                                                         Homo Sapiens
E: Brain
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83.3%;
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Pred. No. 2.5e+02;
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US-07-956-700B-107
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5252466-6
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5252466-6
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Best Local Similarity
Watches 5; Conserve
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APPLICANT: CRONAN, JOHN E.

TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
;VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
;PURIFYING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107, Application US/07956700B Patent No. 5539092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                              COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-POS/MS-POS
SOFTWARE: ASCII-POS
SOFTWARE: ASCII-POS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,700B
FILING DATE: 19921002
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                TELEPHONE: 1-312-744-00
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 18 MAY-1990
PRIOR APPLICATION DATA;
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                             REFERENCE/DOCKET NUMBER: AR TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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321 No. 5539092th Clark Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-CoA
VENTION: Carboxylase
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83.3%;
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83.3%;
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Pred. No. 2.7e+02;
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Pred. No. 2.6e+02;
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SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
HOLECULE TYPE: Peptide
US-08-476-537-107
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TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-107
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RESULT 40
US-08-485-607-107
; Sequence 107, Application US/08485607
; Patent No. 5792627
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US-08-476-537-107
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Best Local Similarity 83.9
Matches 5; Conservative
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Patent No. 5756290
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                                                                                                                                                                                             Query Match
Best Local :
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GEMERAL INFORMATION:
APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TITLE OF INVENTION: Carboxylase
"""" OF SEQUENCES: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY,AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,266
REFERENCE/DOCKET NUMBER: ARCD:058
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 1-312-744-00
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,537
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32 GGGTGG 37
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nes 5; Conserv
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Pred. No. 3e+02;
0; Mismatches
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STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-485-607-107
Search completed: February 4, 2002, 08:01:36 Job time: 80 sec
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEPAX: 1-312-755-4489
INFORMATION FOR SEO ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
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ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

MEDIUM TYPE: IBM PC Compatible

"""" PC-DOS/MS-DOS
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APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coa
TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/485,60
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
NAME: Thomas E. No. 5792627thrup
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STREET: Chicago
CITY: Chicago
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CURRENT APPLICATION DATA:
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321 No. 5792627th Clark Street
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83.38;
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Pred. No. 3e+02;
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2000 Com
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A:Molecule type: DNA
A:Residues: 1-279 <WIL>
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                                                                                  A:Reference number:
A:Accession: T26555
                                                                                                                       R:Gardner, A. submitted to the EMBL
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R;Sirito, M.; Walker, S.; Lin, Q.; Kozlowski, M.T.; Klein, W.H.; Sawadogo, M. Gene Expr. 2, 231-240, 1992
Gene Expr. 2, 231-240, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             upstream stimulatory factor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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154074
                                                                                                                                                                          h/pothetical protein Y22F5A.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Residues: 1-234 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Members of the USF family of helix-loop-helix proteins bind DNA as homo-A;Reference number: I54074; MUID:93082094
A;Accession: I54074
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k;Accession: S00739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X07500; NID:g44619; A;Note: the authors translated the codon CAG
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           Cross-references: EMBL:AL021479; PIDN:CAA16324.1; GSPDB:GN00023;
                                                                  Status: preliminary; translated
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Experimental source: clone
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L. 27, 65-76, 1988
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Pred. No. 73;
D; Mismatches
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                                                                  GB/EMBL/DDBJ
                                                                                                                                                                      15-Oct-1999 #text_change
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A; Molecule type: DNA
A; Residues: 1-303 <BEV>
A; Cross-references: EMB
                                                                                                                                          C;Accession: T48493
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, i
                                                                                                                                                                                                                hypothetical protein T28J14.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                        RESULT
T48493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable GT-1-like transcription factor [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein Fi6N4.1B C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001 C;Accession: T01257; G84802 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, July 1998 A;Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.
A; Experimental source:
                                                                                  A; Status: preliminary
                                                                                                           A; Reference number: Z24493
A; Accession: T48493
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A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vannken, S.E.; Umayam, L.; Tallon,
Guss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-289 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euss, D.; Nierman, W.C.; White, O.; Eisen, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-289 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: Arabidopsis
A; Reference number: Z14213
A; Accession: T01257
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A; Introns: 142/3
C; Superfamily: Cae
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A:Map position: 2
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                    EMBL: AL163652
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Pred. No. 86;
D; Mismatches
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Pred. No. 89;
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  BAC
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                                                                                                                                                      S.; Bancroft,
April 2000
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  clone T28J14
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A; Molecule type: mRNA
A; Residues: 1-563 <CHE>
A; Cross-references: EMBL: X72617; NID: g288115; PID: g288116
C; Superfamily: alcohol oxidase
                                                                                                 A; Description: Nucle
A; Reference number:
A; Accession: S32156
C;Superfamily: alcohor oxide
C;Keywords: aldehyde-lyase;
                                                                                                                                                                                              mandelonitrile lyase (EC 4.1.2.10) - black cherry C:Species: Prunus serotina (black cherry) C:Species: 22-Nov-1993 #sequence_revision 13-Mar-1997
                                                                                                                                                  R;Cheng, I.P.; Poulton, submitted to the EMBL Da
                                                                                                                                                                      C; Accession: S32156
R; Cheng, I.P.; Poul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Drosophila melanogaster
C; Date: 10-Nov-1995 #sequence_revision 10-Nov-1995
C; Accession: A57215; A57216
R; Hosoya, T; Takizawa, K.; Nitta, K.; Hotta, Y.
Cell 82, 1025-1036, 1995
A; Title: glial cells missing: a binary switch betwe
A; Reference number: A57215; MUID:96016097
                                                                                     A; Status: preliminary
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C;Keywords: nucleus
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C;Genetics:
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A57215
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A; Residues: 1-504 <HOS>
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A:Introns: 67/1; 152/3; 201/3
A:Note: T28J14.160
C:Superfamily: Arabidopsis thaliana hypothetical protein PL09039.6
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an, C.S.
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93;
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phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor C;Species: Staphylococcus aureus C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Oct-1999 C;Accession: B28474 R;Breidt Jr., F.; Hengstenberg, W.; Finkeldei, U.; Stewart, G.C. J. Biol. Chem. 262, 16444-16449, 1187
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B28474
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Best Local Similarity
"~+~hes 6; Conserv?
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A;Title: Cloning and sequencing of rat liver cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                 glucokinase regulator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Dec-1994 #sequence_revision 26-May-1995 #text_change
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S32494
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A; Residues: 1-569 <DET>
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A; Accession: S32494
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A; Residues: 1-568 <DEV>
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phosphotransferase system enzyme II (EC 2.7.1.69) - La C. Species: Lactobacillus casei C.Date: 04-Oct-1991 *te C.Date: 04-Oct-1991 *te C.Accession: B23697 R.Accession: B23697 R.Alpert, C.A.; Chassy, B.M. J Biol. Chem. 265, 22561-22568, 1990 A. Title: Molecular cloning and DNA sequence of lacE, to n:ial for sugar phosphorylation.

A. Reference number: A23697; MUID:91093108 A. Accession: B23697
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A,Residues: 1-577 <ALP>
A,Residues: 1-577 <ALP>
A,Cross-references: GB:M60851; NID:g149561; PIDN:AAA72984.1; PID:g149563
C,Keywords: phosphotransferase; transmembrane protein
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Accession: B28474
Molecule type: DNA
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Cross-references: GB:J03479;
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Pred. No. 1.7e+02;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 2;
Pred. No. 1.7e+02;
; Mismatches 0;
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Pred. No. 1.7e+02;
; Mismatches 0;
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glucokinase regulator - human (;Species: Homo sapiens (man) (10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (;Accession: $52485 R;Bonthron, D.T.; Intody, S.; Warner, J.P. submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: At2g42580
A;Gene: At2g42580
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A; Residues: 1-578 <SCH>
A; Cross references: EMBL: AL353822; GSPDB: GN00112;
A; Cross references: cosmid contig 15E6; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T48795
C;Accession: T48795
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.;
submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                             RESULT
S52485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, ..., M.; Koo, H.; Moffat, K.S.; Cronin, Leuss, D.; Nierman, W.C.; White, O.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                origin recognition complex subunit 2 related protein [imported] - Neurospora N;Alternate names: protein 15E6.30 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000 C;Date: 05-May-2000
                                    A; Description: Human glucokinase. A; Reference number: S52485 A; Accession: S52485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein At2942580 [Imported] - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change C;Accession: F84855
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A; Accession: T48795
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A; Residues: 1-618 <STO>
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A;Map position: 2
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A; Molecule
                 A;Status: preliminary
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Best Local Similarity
Matches 6; Conserv
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type:
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mRNA
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Pred. No.
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Pred. No. 1.8e+02;
; Mismatches 0;
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1.7e+02;
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A; Molecule type: DNA
A; Residues: 1-629 <KLI>
A; Cross-references: GB: X05418; NID: g34040; PIDN: CAA28991.1; PID: g34041; GB: X05419; NID: g34047
A; Rote: the authors translated the codon AAC for residue 63 as Asp and ACA for residue 2 A; Note: the complete translation is not annotated in GenBank entries HSKER65A, HSKER65B, S mistranslated as a Met initiator codon
C; Genetics:
                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucokinase regulator - rat C.Species: Rattus norvegicus (Norway rat) C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S41745 R;Octheux, M.; Vandekerckhove, J.; van Schaftingen, E. FEBS Lett. 339, 312-315, 1994 A;Title: Cloning and sequencing of rat liver cDNAs encoding the regulatory protein of A;Reference number: S41745; MUID:94156054 A;Accession: S41745; MUID:94156054
                                                                                                                                                                                                                                                                                                                                            R;Klinge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M. J. Mol. Evol. 24, 319-329, 1987
A;Title: Evolution of keratin genes: different protein domains A;Reference number: A29666; MUID:87254239
                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: A29666
                                                                                                                                                                                                                                                                                                                                                                                                                    keratin, 65K type II cytoskeletal - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec:1988 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000
C;Accession: A29666
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A; Residues: 1-627 <DET>
C; Superfamily: glucokinase regulator
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C;Superfamily: glucokinase regulator
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A:Map position: 2p23.3-2p23.2
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A;Cross-references: EMBL:Z48475; NID:g683571; PIDN:CAA88367.1; PID:g683572
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Best Local S
Matches 6
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Best Local
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Pred. No. 1.9
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Pred. No. 1.9
0; Mismatches
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                                             DB 2; I
1.9e+02;
hes 0;
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endopeptidase Clp (EC 3.4.21.-) ATP-binding chain cd4B, chloroplast N;Alternate names: ATP-dependent Clp proteinase regulatory chain B; N;Contains: adenosinetriphosphatase (EC 3.6.1.3) C;Species: Lycopersicon esculentum (tomato) C;Date: 30-un-1993 #sequence_revision 30-Jun-1993 #text_change 19-J C;Accession: B35905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein ZK662.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-668 <CHE>
A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35411.1; PID:g1780830
A;Note: possible protein-coding frames are given
A;Note: the DNA sequence was submitted to EMBL, December 1989, in computer-
C;Superfamily: varicella-zoster virus gene 26 protein
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A; Introns: 30/1; 56/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-780 <WIL>
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Best Local Similarity
Watches 6; Conserve
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Curr. Top. Microbiol. Immunol. 154, 125-169, A; Title: Analysis of the protein-coding conte A; Reference number: S09749; MUID:90269039 A; Accession: S09815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: S09815
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C:Species: human cytomegalovirus, human
A;Note: host Homo sapiens (man)
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Best Local S
Matches 6
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                    98/3; 176/3;
                                                                                                                                                                                                                                                                                                                                                                                                                               clone
                                                                                                                                                                                                                                                                             100.0%;
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Pred. No. 2.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.; Bohni, R.; Brown,
                                                                                                                                                                                                                                                                                                                                                    206/3; 289/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                DB 2;
2.3e+02;
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2e+02;
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                                                             [similarity]
CD4B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
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#text_change 19-Jan-2001

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A:Title: Conservation of the regulatory subunit for the Clp ATP-dependent A:Accession: B35905; MUID:90239044
A:Reference number: A35905; MUID:90239044
A:Accession: B35905
A:Molecule type: DNA
A:Residues: 1-923 <GOT>
A:Cross-references: Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Cd4B
A;Map position: 12
C;Function:
A;Map position: allows clpP to hydrolyze polypeptides and proteins, probably by a (expectipation: allows clpP to hydrolyze polypeptides and proteins but not of: A;Description: allows clpP to hydrolyze polypeptides and proteins but not of: A;Description: allows clpP to hydrolysis of proteins but not of: C;Superfamily: endopeptidase C]B ATP-binding chain chaperone; nucleotide binding molif A (P-loop)
F;300-307/Region: nucleotide-binding motif B
F;643-650/Region: nucleotide-binding motif B
F;711-715/Region: nucleotide-binding motif B
F;711-715/Region: nucleotide-binding motif B
F;711-715/Region: nucleotide-binding motif B
F;711-715/Region: nucleotide-binding motif B
F;306/Binding site: ATP (Lys) #status predicted
F;649/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                 A. Description: allows clpP to hydrolyze polypeptides and proteins, probably e activity; ATP hydrolysis is required for Clp hydrolysis of proteins but no C. Superfamily: endopeptidase Clp ATP-binding chain C. Keywords: ATP; chloroplast; hydrolase; molecular chaperone; nucleotide bin F, 302-309/Region: nucleotide-binding motif A (P-loop) F, 367-371/Region: nucleotide-binding motif B F, 646-653/Region: nucleotide-binding motif A (P-loop) F, 311-715/Region: nucleotide-binding motif A (P-loop)
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A:5905
A:5905
A:600peptidase Clp (EC 3.4.21.-) ATP-binding chain cd4A, chloroplast [similarity]
N:Alternate names: ATP-dependent Clp proteinase regulatory chain A; CD4A protein
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Lycopersicon esculentum (tomato)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 19-Jan-2001
C:Accession: A35905
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: cd4A
A; Map position: 3
C; Function:
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C;Genetics:
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A; Residues: 1-926 <G
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A;Title: Conservation of the regulatory subunit for the Clp ATP-dependent proteas A;Reference number: A35905; MUID:90239044
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C;Genetics:
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                                                                                                                                                                                                                652/Binding site: ATP
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Pred. No.
                                                                                                        Score 33; DB 1; |
Pred. No. 2.7e+02;
; Mismatches 0;
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A; Residues: 1-1192 <WIL1>
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                      A; Molecule type: DNA
A; Residues: 1-130 <SIM>
A; Cross-references: GB:
                                                                                                                                                                                          R;anonymous, The Xylella fastidiosa Nature 406, 151-157, 2000
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A; Experimental source:
                                                                                    A;Status: preliminary
                                                                                                        A;Note: for a complete list of A;Accession: E82669
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probable serine/threonine-specific protein kinase (EC 2.7.1.-), N;Contains: probable serine/threonine kinase, short splice form C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change C;Accession: T18611; T18610; T23144; T23143
R;MCMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; C;Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-487,536-1192 <WIL4>
A;Cross-references: EMBL:Z96102; PIDN:CAB54262.1;
A;Experimental source: clone H39E23
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A;Residues: 1-1192 <WIL3>
A;Cross-references: EMBL:296102; PIDN:CAB54263.1;
A;Experimental_source: clone H39E23
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                                                                                                                                                                                                                                                                                                                              30S ribosomal protein S9 xF1536 [imported] - Xylella fastidiosa (strain 9a5) C;Species: Xylella fastidiosa (C;Date: 1B-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: E82669
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A; Residues: 1-487,536-1192 <WIL2>
A; Cross-references: EMBL: Z81027; PIDN: CAB54178.1;
A; Experimental source: clone AH10
                                                                                                                                                                                                   A; Title: The genome sequence of the plant pathogen A; Reference number: A82515; MUID: 20365717
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A;Map position: 5
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GB:AE003983; GB:AE003849; NID:g9106567; PIDN:AAF84345.1; GSPDB:GN
be: strain 9a5c
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Pred. No.
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                                                                                                                                                                                reference
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hes 0;
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submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frobus A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigy J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigy Chado, M.A.; Madeira, A.M.B. N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marcins, E.A.; Miyaki, C.Y.; A; Marcins: E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; Med Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein b2674 - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S70890; C65047 R;Jordan, A.; Aragall, E.; Gibert, I.; Barbe, J. Rol. Microbiol. 19, 777-790, 1996 A;Title: Promoter identification and expression ana A;Reference number: S70890; MUID:96417857 A;Accession: S70890
hypothetical protein nrdI [imported] - Escherichia coli (strain C;Species: Escherichia coli (C;Species: Escherichia coli C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change C;Accession: D85915 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner,
                                                                                                                                RESULT
D85915
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000352; GB:U00096; NID:g1789024; PIDN:AAC75721.1; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: Bacillus subtilis conserved hypothetical protein yosM
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A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: C65047
A;Status: preliminary; nucleic acid sequence not show A;Status: preliminary;
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A; Contents: annotation
C; Genetics:
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A; Residues: 1-136 <BLAT>
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C; Superfamily:
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Best Local
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Pred. No. 1.4e
1; Mismatches
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Pred. No. 1.4e+02;
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J.D.; Rose,
                                                 31-Mar-2001
                                                                                                   O157:H7)
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A; Molecule type: I
A; Residues: 1-185
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hypothetical protein Vng0219h [imported] -
C:Speckes: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-F
C:Accession: F84182
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A;Introns: 105/1; 114/1
A;Note: T2J13.80
C;Superfamily: Escherichia
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y;Alternate names: protein T2J13.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: ^- ~~~-2nAn #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
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A;Reference number: A84160; MUID:20504483
A;Accession: F84182
A;Status: preliminary
                                                                                                        R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
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A;Accession: T46122
A;Status: preliminary
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A; Residues: 1-136 <STO>
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                                                                A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; A; Title: Genome sequence of Halobacterium species NRC-1.
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A; Residues: 1-143 <RIE>
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Best Local
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A85480; MUID:21074935; PMID:11206551
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Pred. No. 1.
1; Mismatche
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Pred. No. 1.4e+02;
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1.5e+02;
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glycine-rich protein grp3 - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_rev
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S56827
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C;Genetics:
A;Gene: VNG0219H
RESULT
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A:Title: Root-specific expression of a Zea mays gene encoding a A:Reference number: Z14904; MUID:98187261
A:Accession: T03371
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C:Superfamily: yeas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Date: 08-Jul-1995 #sequence_revision
C:Accession: S56827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1148
C:Species: Saccharomyces cerevisiae
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A: Residues: 1-245 < TOV>
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A:Residues: 1-256 <GOD>
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A:Accession: S56827
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Matches 5
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Best Local
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Best Local
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30
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                                                                 1 GGGTSG
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5; Conserv
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5; Conservative
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                                                                                               Conservative
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                                                                                                          90.9%;
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                                                                                                         Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30;
Pred. No.
                                                                                            Mismatches
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2.5e+02;
0;
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. 1.9e+02;
. 0;
                                                                                       DH 2,
2.6e+02;
0;
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                                                                                                                        Length 256;
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                                                                                                                                                                                                                     PID:g1532071
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                                                             C; Accession: E65020 R; Blattner, F.R.; Plunkett III,
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-278 <STO>
A; Cross-references: GB:
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Gene: eutJ
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Best Local
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|145 GGGTTG 15
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5; Conserv
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R;Biacure, D.J.; Mau, B.; Snao, ...
A.; Rose, D.J.; Mau, B.; Snao, ...
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Nolecule type: DNA
A:Residues: 1-276 <WHI>
A:Cross references: GB: AE002055;
A:Cross references: Strain R1
                                                                                                                                                               C;Species: Escherichia coli
C;Date: 12-Sep-1997 *sequence_revision 17-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                          ethanolamine utilization protein EutJ -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein eutJ [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: G85887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 286, 1571-1577, 1999
A;Tiltle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896
A;Accession: F75300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE005174; NID:g12516826; PIDN:AAG57563.1; ce: strain O157:H7, substrain EDL933
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Pred.
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Pred. No. 2.8e+02
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2.8e+02;
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, L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 278;
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anta, E.; Potamousis,
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T.; Z
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                                                                                                                     Riley,
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K.; Apoda
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A;Reference number: JC6502; MUID:98
A;Accession: JC6502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: I-310 <BRU>
A;Cross-references: GB:AF002241; N1
C;Keywords: carbon-oxygen lyase
       В
                                 γQ
                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-340 <WIL>
                                                                                                                                                                                                                                                                                                                                    hypothetical protein F13A7.1 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Accession: T20807
                                                                                                                                       A; Map position: 5
A; Introns: 6/2; 44/2;
                                                                                                                                                                                                             A; Cross-references: EMBL: Z93377; PIDN: CAB07573.1; GSPDB: GN00023;
                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z19327 A; Accession: T20807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pectate lyase (EC 4.2.2.2) - Amycolata sp.
(;Species: Amycolata sp.
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: JC6502
R;Bruchlmann, F.; Keen, N.T.
Gene 202, 45-51, 1997
A;Title: Cloning, sequence and expression of the pel gene from an Amycolata A;Reference number: JC6502; MUID:98087416
                                                                                                                                                                        A; Gene: CESP:F13A7.1
                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                                         R; McMurray, A.
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Best Local Similarity
"arches 5; Conserve
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Best Local S
Matches 5
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Best Local
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nes 5; Conser
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                                    1 GGGTSG 6
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       GGGTAG 229
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                                                                 Similarity
5; Conser
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                                                               Conservative
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                                                            Score 30; DB
Pred. No. 3.4e
1; Mismatches
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Pred.
1; Mis
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Pred. No. 2.
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                                                       DB 2;
3.4e+02;
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3.1e+02;
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2.8e+02;
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                                                                                         Length 340;
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B34261
A; Reference number: A34261; MUID:90254112
A; Accession: B34261
                           ndent dehydrogenases.
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A; Molecule type: DNA
A; Residues: 1-364 <SAU>
A; Cross-references: EMBL: AL109663; |
A; Cross-references: Strain A3(2)
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Best Local Similarity
"atches 5; Conserve
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C; Superfamily:
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submitted to the EMBL Data Lik
A;Reference number: 221563
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T34954
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family: murG protein
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                                                                                                                                                                                                                                                                      Conservative
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C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I57555
R;Kurschner, C.; Morgan, J.I.
Mol. Cell. Biol. 15, 246-254, 1995
Mol. Cell. Biol. 15, 246-254, 1995
A;Title: The maf proto-oncogene stimulates transcription from multiple site
A;Reference number: I57555; MUID:95097997
R;Kuroda, S.; Tanizawa, K.; Sakamoto, Y.; Tanaka, H.; Soda, K.
Biochemistry 29, 1009-1015, 1990
A;Title: Alanine dehydrogenases from two Bacillus species with distinct thermostabili
                                                                             C;Species: Bacillus stearothermophilus
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 11-Jun-1999
C;Accession: B34261
                                                                                                                                                alanine dehydrogenase (EC 1.4.1.1) - Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: maf transforming protein; maf homology F;259-348/Domain: maf homology <MAF>
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C;Date: 05.Nov-1999 *sequence_revision 05-Nov-1999 *text_change 21-Jan-2000
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C;Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                       90.9%;
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83.3%;
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Library, August 1999
                                                                                                                                                                                                                                                                                                                                                              Score 30; DB
Pred. No. 3.76
1; Mismatches
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Pred. No.
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A.Gene: lmx-1

A.Gene: lmx-1

C.Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat homology: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc c; Keywords: DNA binding; duplication; phomeobox; nucleus; transcription regulation; zinc r; 35-85/Domain: LIM metal-binding repeat homology <LIMI>
F; 94-147/Domain: LIM metal-binding repeat homology <LIM2>
F; 196-252/Domain: homeobox homology <HOX>
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A;Molecule type: DNA
A;Cross-references: GB:M33299; NID:g142454; PIDN:AAA22211.1; PID:g142
C;Superfamily: alanine dehydrogenase; alanine dehydrogenase homology
C;Keywords: NAD; oxidoreductase
F;1-277/Domain: alanine dehydrogenase homology <ALA>
F;170-198/Region: beta-alpha-beta NAD nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:X81406; NID:g587460; PIDN:CAA57163.1; PID:g587461 A;Experimental source: insulinoma cell line HIT T-15 M2.2.2 A;NOTE: sequence extracted from NCBI backbone (NCBIN:117927, NCBIP:11792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Synergistic activation of the insulin gene by a LIM-homeo A;Reference number: A46233; MUID:93051335
A;Accession: B46233
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: B46233
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                  A; Map position: 3
A; Introns: 313/3
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A; Residues: 1-382 <RIE>
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A; Residues: 1-382 <GER>
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A; Note:
                                                                                      A; Experimental source:
                                                                                                             A; Cross-references: EMBL: AL138648
                                                                                                                                                                            A; Status: preliminary
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175 GGGTAG 180
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nes 5; Conser
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pred. No. 3.8e+02;
pred. No. 3.8e+02;
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Pred. No. 3.7e+02;
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstehn, G.; Kroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino a;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauy, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl a;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Winters, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12607.1; PID:e11827
A;Experimental source: strain 168
C;Genetics:
A;Gene: yfkR
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change 15-Oct-1999
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A; Residues: 1-384 <KUN>
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Pred. No. 3.8e+02;
1; Mismatches 0
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3.8e+02;
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